

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:00:20 ; Search time 13.566 Seconds
(without alignments)
339.796 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586

Perfect score: 332

Sequence: 1 CSLSNGAHGSDGPCNNNTSC.....CDITEYCTGD;GQCPEPLMK 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283306

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	213	64.2	524	2	S38539	disintegrin-like m
2	213	64.2	524	2	S38539	disintegrin-like m
3	168.5	50.8	814	2	G02350	disintegrin-like m
4	168	50.6	617	2	S48160	metalloproteinase
5	153	46.1	357	2	S23403	sperm surface prot
6	153	46.1	736	2	S47645	WDC I protein - c
7	152	45.8	734	2	JC4861	ferillin beta cha
8	151	45.5	735	2	G02937	ferillin beta - cr
9	148	44.6	600	2	I49281	ferillin alpha pre
10	147	44.3	616	2	A55796	ecarin precursor -
11	146.5	44.1	419	2	A59414	metalloproteinase
12	145.5	43.8	571	2	S24789	farahagin C precu
13	145.5	43.8	609	2	S55270	catrocollastratin p
14	144	43.4	825	2	S55060	ferillin alpha-II
15	144	43.4	905	2	S55059	ferillin alpha-I -
16	143	43.1	150	2	S60258	meltrin beta - mou
17	136	41.0	473	2	I49283	ADAM 4 protein pre
18	136	41.0	549	2	S48169	metalloproteinase
19	136	41.0	823	2	S18968	cyrtloestatin precu
20	135	40.7	610	2	JC7530	vascular apoptosis
21	134	40.4	416	2	A57877	hemorrhagic protei
22	134	40.4	903	2	S60257	meltrin alpha - mo
23	134	40.1	952	2	T18900	disintegrin and me
24	133	39.8	216	2	JX0265	platelet aggregati
25	132	39.8	789	2	S28259	androgen-regulated
26	130	39.2	655	2	JC7850	disintegrin and me
27	130	39.2	660	2	ST1949	metalloproteinase
28	130	39.2	732	2	I52361	extracellular metallo
29	129.5	39.0	209	2	JX0266	platelet aggregati

30	129	38.9	735	2	I48101	ADAM 6 protein pre
31	128	38.6	777	2	I48100	ADAM 5 protein pre
32	127.5	38.4	419	2	S41607	acetylserin A (EC 3.
33	122	36.7	429	2	A42972	coagulation factor
34	122	36.7	723	2	I65253	disintegrin-like t
35	121.5	36.6	733	2	D35982	triglycerin beta-2 -
36	121.5	36.6	478	2	JC4880	fibronolytic metal
37	121	36.4	776	2	S28258	androgen-regulated
38	120.5	36.3	1042	2	T26644	hypothetical prote
39	119	35.8	826	2	A60385	monocyte surface a
40	117	35.2	151	2	S60259	meltrin gamma - mo
41	115	34.6	756	2	S47656	UWDC II protein -
42	113.5	34.2	71	2	A59411	platelet aggregati
43	113.5	34.2	73	2	A59410	platelet aggregati
44	113	34.0	512	2	T37819	probable zinc meta
45	112.5	33.9	71	2	A59409	platelet aggregati

ALIGNMENTS

RESULT 1

S38539 disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 1 - human

N:Alternate names: ADAM11; MDC

C:Species: Homo sapiens (man)

C>Date: 07-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 26-May-2000

C/Accession: S38539; I52965;disintegrin-like gene at 17q21.3 is somatically rearran

R/Eml, M.; Katagiri, T.; Harada, Y.; Saito, H.; Inazawa, J.; Ito, I.; Kasumi, F.; Nakamu

Nature Genet. 5, 151-157, 1993

A>Title: A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearran

A/Reference number: S38539; WUID:94073190; PMID:8252040

A/Accession: S38539

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-524 <EMI>

A/Cross-references: GB:D17390; NID:9452188; PIDN:BA04213.1; PID:di004732; PID:9484255

R/Katagiri, T.; Harada, Y.; Eml, M.; Nakamura, Y.

Cyogenet. Cell Genet. 68, 39-44, 1995

A>Title: Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and

A/Reference number: I52965; WUID:95044425; PMID:7956356

A/Accession: I52965

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 7-225 'D' 227-524 <KAT>

A/Cross-references: GB:D181872; NID:9505090; PIDN:BA06671.1; PID:di007243; PID:9836684

C/Comment: For an alternative splice form, see PIR:I65967.

C/Genetics:

A/Gene: GDB:MDC; ADAM11

A/Cross-references: GDB:230267; OMIM:155120

A/Map position: 17q21.3-17q21.3

A/Intons: 28/3; 57/2; 82/3; 105/1; 127/3; 152/3; 176/3; 232/2; 260/3; 291/1; 308/2; 341/

C/Superfamily: disintegrin homology

C/Keywords: alternative splicing; hydrolase; metalloproteinase

F:344-427/Domain: disintegrin homology <DIS>

Query Match 64.2%; Score 213; DB 2; Length 524;

Best Local Similarity 65.5%; Pred. No. 4.9e-14;

Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSLSNGAHGSDGPCNNNTSCLEFQPRGYECRDVAVNECDITEYCTGDSGQCPEPLMK 55

Db 378 CTTTHDMGSDGLCCRR--CKYEPREVSCREAVNECDIATCTGDSGQCPEPLMK 430

RESULT 2

I65967 disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 2 - human

N:Alternate names: ADAM11; MDC

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 17-Mar-2000 #text_change 11-Jan-2002

C/Accession: I65967; S38539

R/Katagiri, T.; Harada, Y.; Eml, M.; Nakamura, Y.

Cytogenet. Cell Genet. 68, 39-44, 1995
 A:Title: Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and
 A:Reference number: 152965; MUID:95044425; PMID:7956356
 A:Accession: 165967
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 7-670 <KAT>
 A:Cross-references: GB:D31872; NID:G505090; PIDN:BA06670.1; PID:G836683
 R:Emi, M.; Katagiri, T.; Harada, Y.; Saito, H.; Inazawa, J.; Ito, I.; Kasumi, F.; Nakami
 Nature Genet. 5, 151-157, 1993
 A:Title: A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearran
 A:Reference number: S88539; MUID:94073190; PMID:8252040
 A:Accession: S88539
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-225, 'N', 227-495, 'PQGRAVWLPPLCOHLMSSARPGGRHQ' <EMI>
 A:Cross-references: GB:D73390; NID:G452188; PIDN:BA04213.1; PID:G484255
 C:Comment: For an alternative splice form, see PIR:S38539.
 C:Genetics:
 A:Gene: GDB:MDC, ADAM11
 A:Cross-references: GDB:230267; OMIM:155120
 A:Map position: 17q21.3-17q21.3
 A:Introns: 28/3; 57/2; 82/3; 105/1; 127/3; 152/3; 176/3; 232/2; 260/3; 291/1; 308/2; 341
 C:Superfamily: disintegrin homology
 C:Keywords: alternative splicing; hydrolase; metalloproteinase
 F:34-427/Domain: disintegrin homology <DIS>

Query Match 64.2%; Score 213; DB 2; Length 670;
 Best Local Similarity 65.5%; Pred. No. 5, 9e-14;
 Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

OY 1 CSLSNGAHCSGDPCCNNTSCLPQPRGYECRDVAVECDITETCTGDSGCCPNNLHK 55
 Db 378 CTLTHDAMCSGDLCCRR--CKYPRGVSCRAVNECDIAETCTGDSGCCPNNLHK 430

RESULT 3
 G02390
 disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
 C:Accession: G02390; PC4263
 R:Herren, B.; Raines, E.W.; Ross, R.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: H01157
 A:Accession: G02390
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-814 <HER>
 A:Cross-references: EMBL:U46005; NID:G1335871; PIDN:AC51112.1; PID:G1335872
 R:McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,
 Biochem. Biophys. Res. Commun. 230, 333-339, 1997
 A:Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM
 A:Reference number: PC4263; MUID:97168871; PMID:9016778
 A:Accession: PC4263
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-461 <MCK>
 A:Experimental source: articular chondrocyte
 C:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
 C:Superfamily: mouse meltrin alpha; disintegrin homology
 C:Keywords: hydrolase; metalloproteinase; zinc
 F:420-503/Domain: disintegrin homology <DIS>
 F:348,352,358/Binding site: zinc (His) #status predicted
 F:349/Active site: Glu #status predicted

Query Match 50.8%; Score 168.5; DB 2; Length 814;
 Best Local Similarity 51.9%; Pred. No. 1, 8e-09;
 Matches 28; Conservative 8; Mismatches 15; Indels 3; Gaps 2;

OY 1 CSLSNGAHCSGDPCCNNTSCLPQPRGYECRDVAVECDITETCTGDSGCCPNNLHK 53
 Db 453 COLRPGACASDGPCCN--COLRPSGWQCRTRCDLPFCPDSSQCPD 504

RESULT 4
 S48160
 metalloproteinase (EC 3.4.24.-) H-I precursor - carpet viper
 N:Contains: disintegrin
 C:Species: Echis pyramicum leakeyi
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jul-2000
 A:Accession: S48160
 R:Paine, M.J.I.; Moura-da-Silva, A.M.; Theakston, R.D.G.; Crampson, J.M.
 Eur. J. Biochem. 224, 483-488, 1994
 A:Title: Cloning of metalloproteinase genes in the carpet viper (Echis pyramicum leakeyi).
 A:Reference number: S48160; MUID:95010025; PMID:7925363
 A:Accession: S48160
 A:Molecule type: mRNA
 A:Residues: 1-617 <PAI>
 A:Cross-references: GB:X78970; NID:G763092; PIDN:CAA55565.1; PID:G763093
 C:Superfamily: mouse meltrin alpha; disintegrin homology
 C:Keywords: hydrolase; metalloproteinase; venom
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-192/Domain: propeptide #status predicted <PRO>
 F:193-617/Product: metalloproteinase H-I #status predicted <MAT>
 F:403-485/Domain: disintegrin homology <DIS>
 F:337/Active site: Glu #status predicted

Query Match 50.6%; Score 168; DB 2; Length 617;
 Best Local Similarity 52.0%; Pred. No. 1, 7e-09;
 Matches 26; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

OY 1 CSLSNGAHCSGDPCCNNTSCLPQPRGYECRDVAVECDITETCTGDSGCCP 50
 Db 436 CKLTPGSCADGECN--OCFRPARETCRRKIDCDVPEYCTGDSGCCP 483

RESULT 5
 S23403
 sperm surface protein PH-30 beta chain precursor - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jun-2000
 C:Accession: S23403; S25696
 R:Boebel, C.P.; Wolfberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
 Nature 356, 248-252, 1992
 A:Title: A potential fusion peptide and an integrin ligand domain in a protein active in
 A:Reference number: S23402; MUID:92204234; PMID:1552944
 A:Accession: S23403
 A:Molecule type: mRNA
 A:Residues: 1-357 <BOI>
 A:Cross-references: EMBL:Z11720
 A:Accession: S25696
 A:Molecule type: protein
 A:Residues: 5-8, 'X', 10-32; 67-88; 125-129, 'X', 131-134, 'X', 136-141, 'X', 143; 154, 'X', 156-161, 'J'
 C:Superfamily: mouse meltrin alpha; disintegrin homology
 C:Keywords: glycoprotein; transmembrane protein
 F:1-1/Domain: signal sequence (fragment) #status predicted <SIG>
 F:5-357/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>
 F:5-87/Domain: disintegrin homology <DIS>
 F:303-323/Domain: transmembrane #status predicted <TM>
 F:78,186,256/Binding site: carbohydrate (Asn) (covalect) #status predicted

Query Match 46.1%; Score 153; DB 2; Length 357;
 Best Local Similarity 44.4%; Pred. No. 3, 4e-08;
 Matches 24; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

OY 1 CSLSNGAHCSGDPCCNNTSCLPQPRGYECRDVAVECDITETCTGDSGCCPNNLHK 54
 Db 38 CRLKSTRCAQGPCN--QCEFKTGEVCRESTDECDLPYCWSSGACQEDLY 89

RESULT 6
 S47645
 TMDC I protein - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000

C:Accession: S47645
R:Barber, H.L.; Perry, A.C.F.; Jones, R.; Hall, L.
Biochem. Biophys. Acta 1218, 429-431, 1994
A:Title: Sequence and expression of a monkey testicular transcript encoding tMDC I, a nc
A:Reference number: S47645; MUID:94325353; PMID:8049267
A:Accession: S47645
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-736 <BAR>
A:Cross-references: EMBL:X76637; NID:9535016; PIDN:CA54083.1; PID:9535017
F:392-477/Domain: disintegrin homology <DIS>
Query Match 46.1%; Score 153; DB 2; Length 736;
Best Local Similarity 45.3%; Pred. No. 5.9e-08;
Matches 24; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
Oy 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITCYCTGDSGCCPPN 53
Db 426 CTLIGFAECGSGPCCNMTCTIYAGHVCRRKSIDCDPEYCNCTSEFCVDPV 478
RESULT 7
fertilin beta chain - human
JC4861
C:Species: Homo sapiens (man)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jan-2000
A:Accession: JC4861
R:Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A:Title: Molecular cloning of the human fertilin beta subunit.
A:Reference number: JC4861; MUID:96295488; PMID:8702389
A:Accession: JC4861
A:Molecule type: mRNA
A:Residues: 1-734 <GUP>
A:Cross-references: GB:U38905; NID:94151118; PIDN:AAD04206.1; PID:94151119
C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: glycoprotein; integrin binding; transmembrane protein
F:382-734/Product: fertilin beta chain #status predicted <NAT>
F:382-467/Domain: disintegrin homology <DIS>
F:448-450/Region: integrin binding #status predicted
F:686-708/Domain: transmembrane #status predicted <TM>
F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 45.8%; Score 152; DB 2; Length 734;
Best Local Similarity 46.2%; Pred. No. 7.5e-08;
Matches 24; Conservative 7; Mismatches 19; Indels 2; Gaps 1;
Oy 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITCYCTGDSGCCPPN 52
Db 418 CRFKAGSNCAGPCCN--CLFMSKERNCRPSFECDLPICNGSSACCPEN 467
RESULT 8
fertilin beta - crab-eating macaque
G02937
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 01-Dec-2000
A:Accession: G02937; S55061
R:Ramazon, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
submitted to the EMBL Data Library, August 1995
A:Reference number: G12615
A:Accession: G02937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-735 <RAM>
A:Cross-references: EMBL:U33959; NID:9998339; PID:9998340
R:Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A:Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A:Reference number: S55059; MUID:95260313; PMID:7741716
A:Accession: S55061

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-722, 'S', 724-735 <PER>
A:Cross-references: EMBL:X77653; NID:9794076; PIDN:CA54733.1; PID:9794077
C:Superfamily: mouse meltrin alpha; disintegrin homology
F:383-468/Domain: disintegrin homology <DIS>
Query Match 45.5%; Score 151; DB 2; Length 735;
Best Local Similarity 46.2%; Pred. No. 9.4e-08;
Matches 24; Conservative 8; Mismatches 18; Indels 2; Gaps 1;
Oy 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITCYCTGDSGCCPPN 52
Db 419 CRFKAGSNCAGPCCN--CLFMSQERVCRRPSFECDLPICNGTSASCPEN 468
RESULT 9
fertilin alpha precursor - mouse (fragment)
I49281
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jun-2000
A:Accession: I49281
R:Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.
Dev. Biol. 169, 378-383, 1995
A:Title: ADAM, a widely distributed and developmentally regulated gene family encoding m
A:Reference number: I48100; MUID:95269891; PMID:7750654
A:Accession: I49281
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-600 <RNS>
A:Cross-references: EMBL:U22056; NID:9965009; PIDN:AAA74920.1; PID:9965010
C:Genetics:
A:Gene: ADAM 1
C:Superfamily: unassigned disintegrins; disintegrin homology
F:246-336/Domain: disintegrin homology <DIS>
F:180/Active site: Guu #status predicted
Query Match 44.6%; Score 148; DB 2; Length 600;
Best Local Similarity 48.1%; Pred. No. 1.6e-07;
Matches 25; Conservative 8; Mismatches 17; Indels 2; Gaps 1;
Oy 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITCYCTGDSGCCPPN 52
Db 277 CTLKEGAGCSGELCCYN--CTFKKGSICRPABDVCDLPYCDGSTQECPPAN 326
RESULT 10
ecarin precursor - saw-scaled viper
A55796
C:Species: Echis carinatus (saw-scaled viper)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 21-Jul-2000
A:Accession: A55796
R:Nishida, S.; Fujita, T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya, H.; Kido, I.; Paine
Biochemistry 34, 1771-1778, 1995
A:Title: cDNA cloning and deduced amino acid sequence of prothrombin activator (ecarin)
A:Reference number: A55796; MUID:95151760; PMID:7849037
A:Accession: A55796
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-616 <NIS>
A:Cross-references: GB:D32212; NID:9717090; PIDN:BA06910.1; PID:9717091
C:Superfamily: mouse meltrin alpha; disintegrin homology
F:404-486/Domain: disintegrin homology <DIS>
F:338/Active site: Guu #status predicted
Query Match 44.3%; Score 147; DB 2; Length 616;
Best Local Similarity 46.2%; Pred. No. 2.1e-07;
Matches 24; Conservative 8; Mismatches 18; Indels 2; Gaps 1;
Oy 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITCYCTGDSGCCPPN 52
Db 437 CKLKPAGCGGECDC--CKKIRAGTECRPARDDCVABCTGQSAECPPN 486

Mon Oct 27 15:28:08 2003

us-09-634-252a-4_copy_532_586.rpr

Page 4

Search completed: October 21, 2003, 10:11:34
Job time : 16.566 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:02:08 ; Search time 37.0126 Seconds
(without alignments)
235.865 Million cell updates/sec

```
Title: US-09-634-252A-4_COPY_532_586
Perfect score: 332
Sequence: 1 CSLSGAHCSDBGPCNNNTSC.....CDITEYCTGDSIGCCPPNLHK 55
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters:  11078633
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_13Jun03:*

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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	332	100.0	540	22	AAE13059
2	332	100.0	696	21	AAV54457
3	332	100.0	696	22	AAU07190
4	332	100.0	696	23	ABB78130
5	332	100.0	832	20	AAV30207
6	332	100.0	832	20	AAV25120
7	332	100.0	832	23	AA847778
8	332	100.0	832	23	ABU56479
9	332	100.0	832	24	ABU56563

10	213	44.2	488	16	AAR67757	Human fetal brain
11	213	64.2	524	16	AAR67758	Human fetal brain
12	213	64.2	760	16	AAR67759	Human fetal brain
13	213	64.2	769	16	AAR75352	Human fetal brain
14	185	55.7	542	22	AAE13058	ADAM-22d1s-Fc fusi
15	185	55.7	853	20	AAE25111	Human MDC2-beta pr
16	185	55.7	829	20	AAE25118	Human MDC2-alpha p
17	185	55.7	867	20	AAE90208	Amio acid sequenc
18	173.5	52.3	709	17	AAE99801	CRII-7 nerve prote
19	168.5	50.8	91	24	ABE97552	Amnio acid sequenc
20	168.5	50.8	522	22	AAE13054	ADAM-15d1s-Fc fusi
21	168.5	50.8	844	22	AAU08749	Human protease pol
22	168.5	50.8	814	23	ABJ05591	Breest cancer-asso
23	168.5	50.8	814	23	ABB08489	Human metalloprote
24	168.5	50.8	855	23	AAU08748	Human protease pol
25	168.5	50.8	855	23	ABB08488	Human metalloprote
26	167	50.3	499	21	AAE07738	A snake venom prote
27	167	50.3	781	21	AAE07743	A snake venom prote
28	167	50.3	790	21	AAE07705	Amnio acid sequenc
29	167	50.3	790	21	AAE07742	A snake venom prote
30	167	50.3	790	22	AAU12273	Human PRO5997 poly
31	167	50.3	790	24	ABU66671	Human PRO polypept
32	167	50.3	790	24	ABU66917	Human secreted/titra
33	167	50.3	790	24	ABU59752	Novel secreted and
34	162	48.8	685	22	ABE64268	Drosophila melanog
35	160	48.2	633	22	ABE07544	Novel human diagn
36	160	48.2	686	23	AAO14360	Human metalloprote
37	160	48.2	802	22	AAE47105	First splice varia
38	160	48.2	802	23	ABE78299	Amnio acid sequenc
39	160	48.2	812	22	ABE00942	Gene 216 alternati
40	160	48.2	812	22	AAE47106	Second splice vari
41	160	48.2	812	23	ABE78300	Amnio acid sequenc
42	160	48.2	812	23	AAU98885	Human protease PR
43	160	48.2	812	23	AAO14377	Human metalloprote
44	160	48.2	812	23	ABU55870	Human 216 protein
45	160	48.2	813	22	AAU9256	Human PRO polypept

ALIGNMENTS

RESULT	1
AAEL13059	AAEL13059 standard; Protein; 540 AA.
XX	
AC	AAEL13059;
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	ADAM-23dis-Fc fusion construct.
XX	
KW	Human; ADAM disintegrin domain; integrin; endothelial cell migration;
KW	angiogenesis; ocular disorder; inflammatory disease; bone resorption;
KW	osteoporosis; restenosis; thrombosis; tissue repair; wound healing;
KW	retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
KW	retrolental fibroplasia; inflammatory bowel disease; rubecosis; uveitis;
KW	arthritis; rheumatism; myocardial infarction; coronary artery disease;
KW	tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;
KW	preclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;
KW	Ig; Fc region; antiinflammatory; osteopathic; vasotropic; thrombolytic
XX	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Unidentified.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..20
FT	/label= IgK_leader_sequence
FT	21..540
FT	/note= "Mature ADAM-23dis-Fc fusion construct"
FT	23..310 "Human ADAM disintegrin"
FT	/note=
FT	34..91
FT	/label= Human_ADAM_disintegrin_domain

FT Region 313..540
FT /note= "Fc region"
XX MO200162905-A2.
XX
XX
PD 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US05701.
XX
XX 25-FEB-2000; 2000US-184865P.
XX
XX (IMMUNEX) IMMUNEX CORP.
XX
XX Fanslow WC, Cerretti DP, Poindexter KM, Black RA;
XX
XX WPI; 2001-625725/72.
XX N-PSDB; AAD21439.
XX
XX Antagonizing the binding of an integrin to its ligand useful for the
FT treatment of angiogenesis comprises administration of an
PT ADAM-disintegrin domain polypeptide
XX
XX Claim 11; Page 60-61; 66pp; English.
XX
XX The invention relates to the method and use of ADAM disintegrin domain
CC polypeptides for inhibiting the biological activity of integrins,
CC endothelial cell migration and angiogenesis. ADAM disintegrin domain
CC polypeptides are used for treatment of ocular disorders, malignant and
CC metastatic conditions, inflammatory diseases, osteoporosis and other
CC conditions mediated by accelerated bone resorption, restenosis,
CC inappropriate platelet activation, recruitment or aggregation, thrombosis
CC or a condition requiring aggregation, thrombosis or a condition requiring
CC tissue repair or wound healing, angiogenesis, ocular neovascularization
CC or solid tumor, diabetic retinopathy, retinopathy or prematurity,
CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubeosis,
CC uveitis, macular degeneration and corneal graft neovascularization,
CC inflammatory diseases, ocular tumors, diseases associated with chorioidal
CC or iris neovascularization, arthritis, rheumatism, inflammatory bowel
CC disease, psoriasis, coronary artery disease or injury, myocardial
CC infarction or injury following myocardial infarction, stroke, unstable
CC angina, atherosclerosis, arteriosclerosis, pre-eclampsia, embolism,
CC platelet-associated ischemic disorders including lung ischaemia,
CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
CC coronary intervention including angioplasty, atherectomy, stent placement
CC and bypass surgery, thrombotic disorders, intracardiac thrombosis,
CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis and
CC coagulopathies associated with exposure to a foreign or injured tissue
CC surface and reocclusion following thrombosis, deep venous thrombosis,
CC pulmonary embolism, transient ischemic attacks and another conditions
CC where vascular occlusion is a common underlying feature, in individuals
CC at high risk for thrombus formation or reformation, advanced coronary
CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis
CC of blood vessels or stroke benign tumors and preneoplastic conditions,
CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular
CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host
CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and
CC wound granulation. The method are used in combination with angioplasty
CC procedures, such as balloon angioplasty, laser angioplasty, coronary
CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of
CC vascular grafts, surgery having a high risk of thrombus formation (i.e.
CC coronary bypass surgery, insertion of a prosthetic valve or vessel and
CC the like), atherectomy, stent placement, placement of a chronic
CC cardiovascular device such as an in-dwelling catheter or prosthetic valve
CC or vessel, organ transplantation or bypass surgery. The present sequence
CC is ADAM disintegrin domain polypeptide fusion construct. The fusion
CC construct comprises of immunoglobulin K (IgK) leader, human ADAM
CC disintegrin and Fc region.
XX
XX Sequence 540 AA:
SQ

Query Match 100.0%; Score 332; DB 22; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-25;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CSLSGAHCSDGPCNNNTSCLPFGRGYECRAVNECDITEXTGDSGCCPNLAK 55
Db 50 CSLSGAHCSDGPCNNNTSCLPFGRGYECRAVNECDITEXTGDSGCCPNLAK 104
RESULT 2
AA554457
ID AA554457 standard; Protein: 696 AA.
XX
XX AA554457;
XX
XX 25-APR-2000 (first entry)
XX
XX
DE Amino acid sequence of a disintegrin homologue designated zdinrl.
XX
XX Human; disintegrin homologue; zdinrl; cardiac myocyte; adipocyte;
XX gene therapy; cell-cell interaction; chondro sarcoma; atherosclerosis;
XX Alzheimer's disease; restenosis; ischemic reperfusion; obesity;
XX intimal hyperplasia; tumor; platelet aggregation; apoptosis;
XX neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
XX connective tissue disorder; chondrogenesis; tumor proliferation;
XX inflammation.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX
XX Domain 1..163
FT /note= "propeptide sequence"
FT 164..382
FT Domain /note= "protease sequence; this sequence is
FT specifically claimed in claim 4"
FT 383..464
FT Domain /note= "disintegrin sequence; this sequence is
FT specifically claimed in claim 5"
FT Misc-difference 437..450
FT /note= "this sequence is specifically claimed in claim 2"
FT 438..449
FT Region /note= "disintegrin loop"
FT 443..445
FT Region /note= "RGD binding loop"
FT 465..696
FT Domain /note= "cysteine-rich domain; this sequence is
FT specifically claimed in claim 6"
XX
XX MO200002912-A2.
XX
XX 20-JAN-2000.
XX
XX 09-JUL-1999; 99WO-US15638.
XX
XX 10-JUL-1998; 98US-0113883.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Baindur N, Delsher TA, Bishop PD;
XX
XX WPI; 2000-160898/14.
XX N-PSDB; AA245826.
XX
XX Polypeptide useful in modulating cell-cell interaction in tissues of
XX heart, brain, spinal cord and treating chondro sarcoma,
XX atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -
XX
XX Claim 7; Page 127-129; 132pp; English.
XX
XX The present sequence represents a human disintegrin homologue, designated
XX zdinrl. The zdinrl polypeptide is a cardiac myocyte proliferation and
XX differentiation stimulator, as well as an adipocyte proliferation and
XX differentiation inhibitor. Polynucleotides encoding zdinrl are used in
XX gene therapy. The zdinrl polypeptide is useful in modulating cell-cell
XX interactions of cells derived from tissues of heart, brain, spinal cord

CC and skeletal muscle. It is useful in treating and diagnosing chondro
CC sarcoma, atherosclerosis, Alzheimer's disease, restenosis, ischemic
CC reperfusion, obesity, intimal hyperplasia and tumors of heart, brain,
CC and spinal cord. The zdin1 polypeptide is also useful in identifying
CC its new family members, antagonists, agonists and antibodies.
CC Antagonists, antibodies and fusion proteins of zdin1 are useful in
CC inhibiting platelet aggregation, apoptosis, neurogenesis and myogenesis.
CC Agonists and antagonists are useful in studying cell-cell interactions,
CC arthritis, myogenesis, neurogenesis, connective tissue disorders,
CC chondrogenesis, tumour proliferation and suppression, extracellular
CC matrix proteins, repair and remodelling of ischemic reperfusion,
CC inflammation, and apoptosis.

XX
XX Sequence 696 AA;
SQ

Query Match 100.0%; Score 332; DB 21; Length 696;
Best Local Similarity 100.0%; Pred. No. 6.6e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITETCTGSGCCPPNLHK 55
Db 409 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITETCTGSGCCPPNLHK 463
|||||

RESULT 3
AAU07190 ID AAU07190 standard; Protein; 696 AA.
XX
XX AAU07190;
AC
XX
XX 04-DEC-2001 (first entry)
DT
XX
XX Human disintegrin protease, zdin1.
DE
XX
XX Human, disintegrin: zdin1; antiangiogenic; vascular; thrombolytic.
KM cell matrix; cell-cell interactions; apoptosis; neurogenesis;
KM connective tissue disorders; chondrogenesis; arthritis;
KM tumour proliferation; ischaemia reperfusion; inflammation;
KM chromosome 2q33.
XX
XX
OS Homo sapiens.

XX
XX Key Location/Qualifiers
FH 1..163
FT /label= Propeptide
FT 164..696
FT /label= Mature_zdin1
FT /note= "This sequence is specifically claimed in
claim 4"
FT /label= Protease region
FT /note= "This sequence is specifically claimed in
claim 1"
FT /label= Disintegrin sequence
FT /note= "This sequence is specifically claimed in
claim 2"
FT 383..696
FT /label= Disintegrin/cysteine-rich sequence
FT /note= "This sequence is specifically claimed in
claim 3"
FT 438..449
FT /label= Disintegrin_loop
FT 443..445
FT /label= RGD_binding_loop
XX
XX US6265199-B1.
XX
XX 24-JUL-2001.
XX
XX 09-JUL-1999; 99US-0351414.
XX
XX 10-JUL-1998; 98US-0092371.

XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Sheppard PO, Bairdur N, Delsher TA, Bishop PD, Taft DW;
PI
XX
XX WPI; 2001-450736/48.
DR
XX
XX N-PSDB; AAS11991.
DR
XX
XX Disintegrin protease zdin1, useful for producing agents for the
PT development of antithrombotic and anti-migration of tumour cells and
PT have antiangiogenic activity -
PT
XX
XX Claim 5; Column 53-56; 50pp; English.
XX
XX
XX The invention relates to an isolated novel disintegrin protease family
XX member, zdin1. Disintegrins bind cell surface molecules, including
XX integrins, on the surface of various cells such as platelets,
XX fibroblasts, tumour, endothelial, muscle, neuronal, bone and sperm cells.
XX Disintegrins are unique and potentially useful tools for investigating
XX cell matrix and cell-cell interactions, apoptosis, neurogenesis,
XX connective tissue disorders, chondrogenesis, arthritis, tumour
XX proliferation, ischaemia reperfusion and inflammation. Additionally, they
XX are useful in the development of antithrombotic and anti-migration of
XX tumour cells and have antiangiogenic activity. The present sequence
XX represents human disintegrin, zdin1, the gene for which is located on
XX chromosome 2q33.
XX
XX
SQ Sequence 696 AA;
QY
Query Match 100.0%; Score 332; DB 22; Length 696;
Best Local Similarity 100.0%; Pred. No. 6.6e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITETCTGSGCCPPNLHK 55
Db 409 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITETCTGSGCCPPNLHK 463
|||||

RESULT 4
ABB78130 ID ABB78130 standard; Protein; 696 AA.
XX
XX
XX ABB78130;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX Amino acid sequence of human zdin1.
DE
XX
XX Human, zdin1; disintegrin protease; platelet accumulation;
KM chromosome 2q33; platelet aggregation; proteolysis; apoptosis;
KM neurogenesis; myogenesis; connective tissue disorder; arthritis;
KM chondrogenesis; cell adhesion; cell fusion; neuron; myocyte; heart;
KM brain; spinal cord; skeletal muscle tissue; Alzheimer's disease;
KM tumour formation; multiple sclerosis; congestive heart failure;
KM ischaemic reperfusion; intimal hyperplasia; restenosis; enzyme.
XX
XX
OS Homo sapiens.

XX
XX Key Location/Qualifiers
FH 164..382
FT /note= "Protease domain"
FT 383..464
FT /note= "disintegrin sequence"
FT 438..449
FT /note= "disintegrin loop"
FT 465..696
FT /note= "cysteine-rich domain"
XX
XX US2002072102-A1.
XX
XX 13-JUN-2002.
XX
XX 16-MAR-2001; 2001US-0809790.

```

XX 10-JUL-1998; 98US-092371P.
PR 09-JUL-1999; 99US-0351414.
XX
PA (SHEP/) SHEPPARD P O.
PA (BAIN/) BAINUR N.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
PI Sheppard PO, Baindur N, Deisher TA, Bishop PD;
XX
XX WPI: 2002-598452/64.
DR N-PSDB; ABQ78447.
XX
PT New disintegrin homolog polypeptide and polynucleotide, useful for
PT modulating cell-cell interactions and diagnosis, treatment of
PT Alzheimer's disease, tumour formation, multiple sclerosis and congestive
PT heart failure
XX
PS Claim 7; Page 29-30; 53pp; English.
XX
CC The present sequence represents a human polypeptide designated zdintl.
CC zdintl is a member of the disintegrin protease family. zdintl inhibits
CC platelet accumulation. The zdintl gene is present on chromosome 2q33.
CC zdintl polypeptides and polynucleotides are useful in treatment of
CC disorders associated with infarct in brain or heart tissue and/or
CC platelet aggregation, to modulate proteolysis, apoptosis, neurogenesis,
CC myogenesis, connective tissue disorders, arthritis, chondrogenesis,
CC cell adhesion, cell fusion, and signalling or to treat or prevent
CC development of pathological conditions in such diverse tissue as heart,
CC brain, spinal cord and skeletal muscle. The molecules modulate
CC inhibition and proliferation of neurons and myocytes in heart, brain,
CC spinal cord and skeletal muscle tissue. Disorders which may be amenable
CC to diagnosis, treatment or prevention with zdintl polypeptides include,
CC Alzheimer's disease, tumour formation, multiple sclerosis, congestive
CC heart failure, ischaemic reperfusion or infarct and degenerative
CC diseases. The zdintl molecules particularly useful in the treatment of
CC intimal hyperplasia or restenosis due to acute vascular injury.
XX
SQ Sequence 696 AA;

```

Query Match 100.0%; Score 332; DB 23; Length 696;
 Best Local Similarity 100.0%; Pred. No. 6.6e-25;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSLSGAHCSGDPCCNNNTSCLFQPRGYECRDVAVNECDITTEYCTGDSGQCPNLRK 55
 DB 409 CSLSGAHCSGDPCCNNNTSCLFQPRGYECRDVAVNECDITTEYCTGDSGQCPNLRK 463

RESULT 5
 ID AAY30207 standard; Protein; 832 AA.
 AC AAY30207;
 XX
 DT 29-OCT-1999 (first entry)
 XX
 DE Amino acid sequence of the human SVPH3-17 protein.
 XX
 KW SVPH3-17; metalloproteinase-disintegrin; human chromosome 2;
 KW human chromosome 7; malignant hyperthermia susceptibility;
 KW Zellweger syndrome; neonatal adrenoleukodystrophy;
 KW infantile Refsum disease; progressive familial intraparietal colichestatis;
 KW mucopolysaccharidosis VII; split hand/foot malformation;
 KW arylglycerogenic right ventricular dysplasia-4; Copock-like cataract;
 KW insulin dependent diabetes mellitus-12; lamellar type ichthyosis;
 KW transient neonatal myasthenia gravis; congenital aculeiform cataract;
 KW juvenile amyotrophic lateral sclerosis;
 KW familial paroxysmal choreoathetosis;
 KW Finnish lethal neonatal metabolic syndrome.
 XX
 OS Homo sapiens.

```

XX MO9941388-A2.
XX
XX 19-AUG-1999.
XX
XX 11-FEB-1999; 99WO-US03016.
XX
XX 11-FEB-1998; 98US-0074310.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Cerretti DP;
XX
XX WPI: 1999-527371/44.
DR N-PSDB; AAZ10207.
XX
PT DNA encoding the SVPH3-13 and SVPH3-17 proteins for detecting
PT disease corresponding to chromosome 7, e.g. Zellweger syndrome
XX
PS Claim 1; Page 8-9; 82pp; English.
XX
CC The present sequence represents a protein designated SVPH3-17, which
CC is a member of the metalloproteinase-disintegrin family. The
CC specification also describes SVPH3-13 proteins. Both sequences can
CC be used to identify human chromosome 2 or 7, and to map genes on these
CC two chromosomes, and also to identify genes associated with certain
CC diseases, syndromes, or other human conditions associated with human
CC chromosome 2 or 7. The disease that correspond to chromosome 7 include
CC malignant hyperthermia susceptibility, Zellweger syndrome, neonatal
CC adrenoleukodystrophy, infantile Refsum disease, progressive familial
CC intraparietal colichestatis, mucopolysaccharidosis VII, and split
CC hand/foot malformation. Diseases associated with chromosome 2 include
CC arylglycerogenic right ventricular dysplasia-4, insulin dependent diabetes
CC mellitus-12, transient neonatal myasthenia gravis, juvenile amyotrophic
CC lateral sclerosis, congenital aculeiform cataract, copock-like cataract,
CC lamellar type ichthyosis, familial paroxysmal choreoathetosis, and
CC Finnish lethal neonatal metabolic syndrome.
XX
SQ Sequence 832 AA;

```

Query Match 100.0%; Score 332; DB 20; Length 832;
 Best Local Similarity 100.0%; Pred. No. 7.8e-25;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSLSGAHCSGDPCCNNNTSCLFQPRGYECRDVAVNECDITTEYCTGDSGQCPNLRK 55
 DB 532 CSLSGAHCSGDPCCNNNTSCLFQPRGYECRDVAVNECDITTEYCTGDSGQCPNLRK 586

RESULT 6
 ID AAY25120 standard; Protein; 832 AA.
 AC AAY25120;
 XX
 DT 26-AUG-1999 (first entry)
 XX
 DE Human MDC3 protein.
 XX
 KW Metalloproteinase-like-disintegrin-like cysteine rich protein; human;
 KW MDC3-alpha; MDC3-beta; MDC3; medical; treatment; diagnosis.
 OS Homo sapiens.
 XX
 PN JP1155574-A.
 XX
 PD 15-JUN-1999.
 XX
 PF 01-DEC-1997; 97JP-0330020.
 XX
 PR 01-DEC-1997; 97JP-0330020.
 XX
 PA (EISA) EISAI CO LTD.

XX WPI; 1999-398071/34.
DR N-PSDB; AAX78438.
XX
XX
PT New protein belonging to MDC gene family - useful in medical
treatment and diagnosis
XX
PS Disclosure; Page 13-16; 17pp; Japanese.
XX
CC This invention describes novel human MDC2-alpha, MDC2-beta and MDC3
CC proteins and their encoding nucleic acids. The products of the invention
CC are useful in medical treatment and diagnosis.
XX
SQ Sequence 832 AA;

Query Match 100.0%; Score 332; DB 20; Length 832;
Best Local Similarity 100.0%; Pred. No. 7,8e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSLSNGAHGSDGPCNNNTSCLFQPRGYECRDVAVNECDITEYCTGTGSGQCPPLAHK 55
Db 532 CSLSNGAHGSDGPCNNNTSCLFQPRGYECRDVAVNECDITEYCTGTGSGQCPPLAHK 586

RESULT 7
AAB47778
ID AAB47778 standard; Protein; 832 AA.
XX
XX AAB47778;
XX
DT 04-MAR-2002 (first entry)
XX
XX ADAM 23.
XX
KM Disintegrin; ADAM 23; metalloproteinase; domain; adhesion; proteolysis;
KM modulator; alpha-v-beta3 integrin; tumour progression; neural tissue;
KM angiogenesis.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Domain 563..570
FT /label= Disintegrin domain
XX
XX
PN MO200174857-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001MO-US10729.
XX
XX 03-APR-2000; 2000US-194164P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Lopez-Otin C, Freijl JMP, Bianchi AB, Miguel SC, Garcia JML;
PI Trail P;
XX
DR WPI; 2002-066298/09.
DR N-PSDB; AAT72025.
XX
XX
PT Nucleic acid encoding a new ADAM family member, designated ADAM 23 is
PT useful to find modulators of its interaction with integrin which can be
PT used to prevent angiogenesis or increase neural growth -
XX
XX
PS Disclosure; Page 38-41; 44pp; English.
XX
XX This sequence shows a cellular disintegrin, ADAM 23, which is a
CC protein having a disintegrin and metalloproteinase domain. This
CC protein can perform both adhesion and proteolysis functions.
CC Modulators of the interaction between ADAM and alpha-v-beta3 integrin
CC are used to inhibit tumour progression or induce growth of neural
CC tissue. These compounds modulate angiogenesis and induction of matrix
CC metalloproteinases facilitating migration of tumour cells and growth of

CC neural tissue.
XX
SQ Sequence 832 AA;

Query Match 100.0%; Score 332; DB 23; Length 832;
Best Local Similarity 100.0%; Pred. No. 7,8e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSLSNGAHGSDGPCNNNTSCLFQPRGYECRDVAVNECDITEYCTGTGSGQCPPLAHK 55
Db 532 CSLSNGAHGSDGPCNNNTSCLFQPRGYECRDVAVNECDITEYCTGTGSGQCPPLAHK 586

RESULT 8
ABU56479
ID ABU56479 standard; Protein; 832 AA.
XX
XX ABU56479;
XX
DT 02-APR-2003 (first entry)
XX
XX
DE Lung cancer-associated polypeptide #72.
XX
XX Lung cancer-associated polypeptide; cytosstatic; emphysema;
XX antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
XX
XX WO200286443-A2.
XX
PD 31-OCT-2002.
XX
XX 18-APR-2002; 2002MO-US12476.
XX
PF 18-APR-2001; 2001US-284770P.
XX
PR 10-MAY-2001; 2001US-290492P.
XX
PR 09-NOV-2001; 2001US-339245P.
XX
PR 13-NOV-2001; 2001US-350666P.
XX
PR 29-NOV-2001; 2001US-334370P.
XX
PR 12-APR-2002; 2002US-372246P.
XX
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
XX
DR N-PSDB; ABX76201.
XX
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
XX
PS Claim 27; Page 243-244; 453pp; English.
XX
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides

CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.

XX Sequence 832 AA;

Query Match 100.0%; Score 332; DB 24; Length 832;
Best Local Similarity 100.0%; Pred. No. 7.8e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSLSNGAHGSDGPCNNNTSCLFOPRGYECRDVANECDITETCTGDSGQCPNHLK 55
Db 532 CSLSNGAHGSDGPCNNNTSCLFOPRGYECRDVANECDITETCTGDSGQCPNHLK 586

RESULT 9

ABUS6563
ID ABUS6563 standard; Protein; 832 AA.

XX AC ABUS6563;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #156.

XX KM Lung cancer-associated polypeptide; cytostatic; emphysema;

XX KM antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;

XX KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO000286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US12476.

XX PR 18-APR-2001; 2001US-284770P.

XX PR 10-MAY-2001; 2001US-290492P.

XX PR 09-NOV-2001; 2001US-339245P.

XX PR 13-NOV-2001; 2001US-350666P.

XX PR 29-NOV-2001; 2001US-34370P.

XX PR 12-APR-2002; 2002US-372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI: 2003-093161/08.

XX DR N-PSDB: ABX76292.

XX CC The invention relates to a method for detecting a lung cancer-associated
XX transcrip in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung
XX cancer-associated polynucleotides and polypeptides are used for
XX identifying a compound that modulates a lung cancer-associated
XX polypeptide, for inhibiting proliferation of a lung cancer-associated
XX cell to treat lung cancer in a patient and for treating a mammal having
XX lung cancer by administering a modulatory compound identified. The
XX methods are useful for treating lung cancer, such as small cell lung
XX cancer, non-small cell lung cancer or other benign or precancerous

CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.

XX Sequence 832 AA;

Query Match 100.0%; Score 332; DB 24; Length 832;
Best Local Similarity 100.0%; Pred. No. 7.8e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSLSNGAHGSDGPCNNNTSCLFOPRGYECRDVANECDITETCTGDSGQCPNHLK 55
Db 532 CSLSNGAHGSDGPCNNNTSCLFOPRGYECRDVANECDITETCTGDSGQCPNHLK 586

RESULT 10

AAR67757
ID AAR67757 standard; Protein; 488 AA.

XX AC AAR67757;

XX DT 25-MAR-2003 (updated)

XX DT 01-AUG-1995 (first entry)

XX DE Human fetal brain MDC protein.

XX KM MDC protein; breast cancer; mamma carcinoma; ovary cancer;

XX KM chromosome-17.

XX OS Homo sapiens.

XX PN EP633268-A2.

XX PD 11-JAN-1995.

XX PF 13-MAY-1994; 94EP-0107487.

XX PR 14-MAY-1993; 93JP-0136602.

XX PR 22-SEP-1993; 93JP-0257455.

XX PR 23-FEB-1994; 94JP-0049904.

XX PR 12-APR-1994; 94JP-0073328.

XX PA (CANC-) CANCER INST.

XX PA (ETSA) EISAI CO LTD.

XX PI Emi M, Nakamura Y;

XX DR WPI: 1995-038478/06.

XX DR N-PSDB: AAQ76119.

XX CC A detailed map of human chromosome-17 was constructed to analyze the
XX chromosome in breast and ovarian cancer tissues. 2 Novel cDNAs
XX (given in AAQ76120-21) were obtained from fetal cerebellum that
XX encoded novel MDC proteins (AAR67758-59, respectively). 5'-RACE and
XX RT-PCR revealed the sequence given in AAQ76122, encoding the MDC given
XX in AAR75552. Sequences common for these clones are given in AAQ76119
XX and AAR6757, respectively. A genomic DNA sequence (AAQ76124) for MDC
XX was obtained from cosmid clone CC117-904.
XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 488 AA;

Query Match 64.2%; Score 213; DB 16; Length 488;

Mon Oct 27 15:28:06 2003

us-09-634-252a-4_copy_532_586.rag

Page 7

Best Local Similarity 65.5%; Pred. No. 2.9e-13;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Oy 1 CSLSNGLHCSDDGPECCNNTSLFPPRGVECRDAVNECDITEYCTDSSGGQCPENLHK 55
::: ||||| ::||| |
Db 371 CTLTHDAMCSDGLCCR--CKYEPRGVSCREAVNECDIAETCTGSSSQCPENLHK 423
::: ||||| ::||| |

```
Search completed: October 21, 2003, 10:08:28
Job time : 38.0126 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:02:08 ; Search time 9.68553 Seconds
(without alignments)
267.045 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586
Perfect score: 332
Sequence: 1 CSLSNGAHCSGPCNNNTSC.....CDITEXCTGDS;GCCPPLHAK 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	64.2	769	AD11_HUMAN	O75078 homo sapien
2	213	64.2	773	AD11_MOUSE	O91144 mus musculu
3	185	55.7	452	AD11_XENLA	O93233 xenopus lae
4	185	55.7	906	AD22_HUMAN	O930K1 homo sapien
5	184	55.4	857	AD22_MOUSE	O93146 mus musculu
6	183	55.1	935	AD22_XENLA	O42336 xenopus lae
7	173.5	52.3	816	AD15_RAT	O93146 mus musculu
8	168.5	50.8	814	AD15_HUMAN	O31444 homo sapien
9	167	50.3	790	AD30_HUMAN	O93146 mus musculu
10	160	48.2	813	AD33_HUMAN	O93146 mus musculu
11	158.5	47.7	815	AD15_MOUSE	O93146 mus musculu
12	153	46.1	735	AD02_CAYPO	O60411 cavia porce
13	152	45.8	735	AD02_HUMAN	O93146 mus musculu
14	152	45.8	751	AD02_RABIT	O28660 corycolagus
15	151	45.5	735	AD02_MACFA	O28478 macaca fasc
16	147	44.3	616	ECAR_ECHCA	O90495 echis carin
17	145.5	43.8	571	DIS1_BORTA	P30431 bothrops ja
18	145	43.7	722	AD21_HUMAN	O93146 mus musculu
19	144	43.4	735	AD02_MOUSE	O93146 mus musculu
20	143	43.1	697	AD26_MOUSE	O93146 mus musculu
21	143	43.1	820	AD29_HUMAN	O93146 mus musculu
22	143	43.1	920	AD19_MOUSE	O35674 mus musculu
23	142	42.8	909	AD12_HUMAN	O93146 mus musculu
24	141	42.5	797	AD33_MOUSE	O93146 mus musculu
25	140.5	42.3	761	AD24_MOUSE	O93146 mus musculu
26	140	42.2	726	AD20_HUMAN	O43506 mus musculu
27	138	41.6	760	AD25_MOUSE	O93146 mus musculu
28	137.5	41.4	737	AD02_RAT	O63202 rattus norv
29	134	40.4	416	HR1B_TRIPL	O20164 trimeresur
30	134	40.4	903	AD02_BOVIN	O77780 bos taurus
31	134	40.4	903	AD12_MOUSE	O93146 mus musculu
32	132.5	39.9	824	AD17_HUMAN	O93146 mus musculu
33	132	39.8	789	AD07_RAT	O63180 rattus norv

ALIGNMENTS

34	132	39.8	956	1	AD19_HUMAN	O90133 homo sapien
35	130.5	39.3	827	1	AD17_MOUSE	O92018 mus musculu
36	130.5	39.3	827	1	AD17_RAT	O921K9 rattus norv
37	130	39.2	776	1	AD28_MACFA	O93146 macaca fasc
38	130	39.2	819	1	AD09_HUMAN	O13443 homo sapien
39	129	38.9	729	1	AD21_MOUSE	O91176 mus musculu
40	129	38.9	788	1	AD07_MOUSE	O35227 mus musculu
41	127	38.3	719	1	AD18_MOUSE	O91517 rattus norv
42	126	38.0	445	1	AD18_RAT	P97776 rattus norv
43	125	38.0	739	1	AD18_HUMAN	O93146 mus musculu
44	125.5	37.8	65	1	DIS1_CERCE	P83041 cerastes ce
45	125	37.7	746	1	AD18_MACFA	O93194 macaca fasc

RESULT 1
AD11_HUMAN STANDARD; PRT; 769 AA.
AC O75078; O14808; O14809; O14810;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADAM 11 precursor (A disintegrin and metalloproteinase domain 11) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein) (MDC).
GN ADAM11 OR MDC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Brain;
RA Sagan K., Ohya Y., Hasegawa Y., Tanaka I.;
RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2 and MDC3: novel human cellular disintegrins highly expressed in the brain.";
RT Biochem. J. 334:93-98(1998).
RL [2]
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Cerebellum;
RA Kasumi F., Katagiri T., Harada Y., Saito H., Inazawa J., Ito I.,
RT "A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearranged in two primary breast cancers.";
RL Nat. Genet. 5:151-157(1993).
RN [3]
RP SEQUENCE OF 106-769 FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain, Breast, Ovary, and Testis;
RX MEDLINE=95044425; PubMed=7956356;
RA Katagiri T., Harada Y., Emi M., Nakamura Y.;
RT "Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and alternative splicing.";
RL Cytogenet. Cell Genet. 68:39-44(1995).
RN [4]
RP FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON CATALYTIC METALLOPROTEIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=MDC-769;
CC Name=Short; Synonyms=MDC-524;
CC IsoId=O75078-1; Sequence=Displayed;
CC IsoId=O75078-2; Sequence=VSP_005472, VSP_005473, VSP_005474, VSP_005475;
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN. SLIGHTLY DETECTED OR NOT AT ALL IN OTHER TISSUES.
CC -1- DOMAIN: A CONSERVED MOTIF (AVN(E/D)CD) WITHIN THE DISINTEGRIN-LIKE DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.
CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY

CC	SIMILARITY).
CC	-I- DISEASE: REARRANGEMENTS OCCUR IN BREAST AND OVARIAN CANCERS WHICH INVOLVE MULTIPLE EXONS AND DISRUPT THE CODING REGION.
CC	-I- SIMILARITY: Belongs to peptidase family M12B.
CC	-I- SIMILARITY: Contains 1 EGF-like domain.
CC	-I- SIMILARITY: Contains 1 disintegrin domain.
CC	-----
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CC	-----
DR	EMBL; AB009675; BAA32352.1; ..
DR	EMBL; D17390; BAA04213.1; ..
DR	EMBL; D31872; BAA06670.1; ..
DR	EMBL; D31872; BAA06671.1; ..
DR	PIR; I65967; I65967.
DR	HSSP; P18619; 1FVL.
DR	MEROPS; M12_976; ..
DR	Gnew; HGNC:189; ADAM11.
DR	MIM; 155120; ..
DR	GO; GO:000586; C:plasma membrane; TAS.
DR	GO; GO:0005178; F:integrin binding activity; TAS.
DR	GO; GO:0007228; F:integrin-mediated signaling pathway; TAS.
DR	InterPro; IPR006586; ADAM_cysteine.
DR	InterPro; IPR001762; Disintegrin.
DR	InterPro; IPR006209; EGF like.
DR	InterPro; IPR002870; Peg_M12B_propep.
DR	InterPro; IPR001590; Reprolysin.
DR	InterPro; IPR006025; Zn_Mrpeptidse.
DR	Pfam; PF00200; disintegrin; 1.
DR	Pfam; PF01562; Peg_M12B_propep; 1.
DR	Pfam; PF01421; Reprolysin; 1.
DR	PRINTS; PR00289; DISINTEGRIN.
DR	Prodrom; PP000664; Disintegrin; 1.
DR	SMART; SMO0608; ACR; 1.
DR	SMART; SMO0050; DISIN; 1.
DR	PROSITE; PS50215; ADAM_MEPRO; 1.
DR	PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR	PROSITE; PS50214; DISINTEGRIN_2; 1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; FALSE_NEG.
DR	PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KW	Signal, Glycoprotein, Transmembrane, EGF-like domain; Alternative splicing.
FT	SIGNAL 1 23
FT	PROPEP 24 225
FT	CHAIN 226 769
FT	DOMAIN 226 734
FT	TRANSMEM 735 755
FT	DOMAIN 756 769
FT	DOMAIN 226 438
FT	DOMAIN 444 531
FT	DOMAIN 532 676
FT	DOMAIN 677 709
FT	DISULFID 349 433
FT	DISULFID 503 516
FT	DISULFID 677 692
FT	DISULFID 686 698
FT	DISULFID 700 709
FT	CARBOHYD 96 96
FT	CARBOHYD 163 163
FT	CARBOHYD 605 605
FT	CARBOHYD 673 673
FT	VARSPLIC 1 99
FT	VARSPLIC 100 104
FT	VARSPLIC 595 623
FT	DYLCFLPLCTNISCAGPRIADLVGDIISVTV -> PQGGAAVW LPPLCDQHLWSSSRSGPGGHQ (in isoform Short).

```

FT FT VASBPIC 624 769 /FtId=VSP_005474. Missing (in isoform Short).
FT FT CONFLICT 106 106 /FtId=VSP_005475.
FT FT CONFLICT 325 325 Q -> H (IN REF. 1) .
FT FT SEQUENCE 769 AA; 83409 MW; 59B9C467B6DFFBEE CRC64; D -> N (IN REF. 2) .
SQ QUERY MATCH Match Local Similarity 64.2%; Score 213; DB 1; Length 769; Pred. No. 3,1e-15; Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Oy 1 CSLISNGAHCSGDPGCCNNTSCIFOPRGYRCRDVAVECDITEXCTGDSDQCPNNLHK 55
Db 477 CTTLDHDMCGSGLCCRR--CKYERGRGSCHAEAVNECIAETICTDDSSQCPCPNLHK 529
|:::||||| |:::||| ||||| |||||
RESULT 2
ID AD11_MOUSE STANDARD; PRT; 773 AA.
AC OPRIV4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM11 precursor (A disintegrin and metalloproteinase domain 11)
DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)
DE (MDC).
GN ADM11 OR MDC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090.
RN [1]
RP SEQUENCE FROM N.A.
RF TISSUE=Brain;
RX MEDLINE=99365303; Pubmed=10433968;
RA Sagane K., Yamazaki K., Mizui Y., Tanaka I.;
RT "Cloning and chromosomal mapping of mouse ADM11, ADM22 and ADM23.";
Gene 236:79-86(1999).
CC -! FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. WEAKLY
CC DETECTED IN THE HEART, LIVER AND TESTIS.
CC -! DOMAIN: A CONSERVED MOTIF [AYN(E/D)CD] WITHIN THE DISINTEGRIN-LIKE
CC DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTERIN RECEPTOR.
CC -! PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -! SIMILARITY: Belongs to peptidase family M12B.
CC -! SIMILARITY: Contains 1 EGF-like domain.
CC -! SIMILARITY: Contains 1 disintegrin domain.
-----
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-----
DR EMBL; AB009676; BAA83384.1; -.
DR HSSP; P18619; 1FLV.
DR MEROPS; M12.976; -.
DR MGD; MG1:1098667; Adam11.
DR InterPro; IPRO06586; ADAM_cysteine.
DR InterPro; IPRO01762; DisIntegrin.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO02870; Pep_M12B_propep.
DR InterPro; IPRO01590; ReptoLyasin.
DR InterPro; IPRO06025; Zn_MTpeptide.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; pep_M12B_propep; 1.
DR Pfam; PF01421; ReptoLyasin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
```

Prodom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR PROSITE; PS00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM MEMPRO; 1. FALSE_NEG.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 DR Signal; Glycoprotein; Transmembrane; EGF-like domain.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 229 BY SIMILARITY.
 FT CHAIN 230 773 ADAM 11.
 FT DOMAIN 230 738 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 739 759 POTENTIAL.
 FT DOMAIN 760 773 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 230 442 METALLOPROTEASE-LIKE.
 FT DOMAIN 448 535 DISINTEGRIN-LIKE.
 FT DOMAIN 536 680 CYS-RICH.
 FT DOMAIN 681 713 EGF-LIKE.
 FT DISULFID 353 437 BY SIMILARITY.
 FT DISULFID 507 520 POTENTIAL.
 FT DISULFID 681 696 BY SIMILARITY.
 FT DISULFID 690 702 BY SIMILARITY.
 FT DISULFID 704 713 BY SIMILARITY.
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 773 AA; 84134 MW; 9A8A125FB3F743BD CRC64;

Query Match 64.2%; Score 213; DB 1; Length 773;
 Best Local Similarity 65.5%; Pred. No. 3.1e-15;
 Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;
 Oy 1 CSLSNGAHCSDGPGCCNNTSCLPQPRGYECRDVAVECDITEYCTGSGCCPPLHK 55
 Db 481 CTLHSDMCMCDGLCCRR--CKYEPBGVSCREAVNECDIAETCTGSGCCPPLHK 533

RESULT 3
 AD11_XENLA STANDARD; PRT; 452 AA.
 AC O9PS23;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE ADAM 11 (A disintegrin and metalloproteinase domain 11)
 DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)
 DE (MDC) (Metalloproteinase-disintegrin MDC11a) (MDC11.1) (Fragment).
 GN ADAM11 OR MDC11a.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=99102794; PubMed=9882486;
 RA Cal H., Kraetzschmar J., Alfandari D., Hunnicutt G., Blobel C.P.;
 RT "Neural crest-specific and general expression of distinct
 RT metalloproteinase-disintegrins in early Xenopus laevis development.";
 RL Dev. Biol. 204:508-524(1998).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: DETECTED IN TESTIS AND BARELY EXPRESSED IN
 CC HEART AND MUSCLE. NOT DETECTABLE IN LIVER.
 CC -1- DEVELOPMENTAL STAGE: COULD NOT BE DETECTED IN EMBRYOS UNTIL
 CC NEURULATION. IN DEVELOPING EMBRYOS, THE EXPRESSION IS RESTRICTED
 CC TO NEURAL CREST DERIVATIVES.
 CC -1- DOMAIN: A CONSERVED MOTIF (AVN(E/D)CD) WITHIN THE DISINTEGRIN-LIKE

CC DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
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 CC -----
 DR EMBL; AF032384; AAC61848.1; -
 DR HSPSP; P18619; 1FVL.
 DR MEROPS; M12; UNB; -
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001590; Reprolysin.
 DR InterPro; IPR006025; Zn_MTPeptidase.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR Prodom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM MEMPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW Glycoprotein; Transmembrane; EGF-like domain.
 FT NON TER 1 1
 FT DOMAIN 1 417 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 418 438 POTENTIAL.
 FT DOMAIN 439 452 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 126 214 METALLOPROTEASE-LIKE.
 FT DOMAIN 215 359 DISINTEGRIN-LIKE.
 FT DOMAIN 360 416 CYS-RICH.
 FT DISULFID 31 115 EGF-LIKE.
 FT DISULFID 186 199 BY SIMILARITY.
 FT DISULFID 360 375 POTENTIAL.
 FT DISULFID 369 381 BY SIMILARITY.
 FT DISULFID 383 392 BY SIMILARITY.
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 452 AA; 48577 MW; DF1F66C24CD6847 CRC64;

Query Match 55.7%; Score 185; DB 1; Length 452;
 Best Local Similarity 56.4%; Pred. No. 1.7e-12;
 Matches 31; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
 Oy 1 CSLSNGAHCSDGPGCCNNTSCLPQPRGYECRDVAVECDITEYCTGSGCCPPLHK 55
 Db 160 CTLHSDMCMCDGLCCRR--GCKYEPBGVSCREAVNECDVPEACPDSACCPPLHK 212
 RESULT 4
 AD22_HUMAN STANDARD; PRT; 906 AA.
 AC O9P0K1; O75075; O75076; O9P0K2; Q9UUA1; Q9UUK2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)

DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein
DE 2) (Metalloproteinase-disintegrin ADAM22-3).
GN ADAM22 OR MDC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20504287; PubMed=11050470;
RA Harada T., Nishie A., Torigoe K., Ikeraki K., Shono T., Maehara Y.,
RA Kuwano M., Wada M.;
RT "The specific expression of three novel splice variant forms of human
RT metalloproteinase-like disintegrin-like cysteine-rich protein 2 gene
RT in brain tissues and gliomas.";
RN Jpn. J. Cancer Res. 91:1001-1006(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RC TISSUE=Brain;
RX MEDLINE=98359734; PubMed=9693107;
RA Sagan K., Ohya Y., Hasegawa Y., Tanaka I.;
RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
RT and MDC3: novel human cellular disintegrins highly expressed in the
RT brain.";
RN Biochem. J. 334:93-98(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 5).
RC TISSUE=Brain;
RA Wada M., Torigoe K., Harada T., Kuwano M.;
RT "Isolation and tissue specific expression of novel ADAM family from
RT 7q21.1 region.";
RN Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 40-906 FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RX MEDLINE=99453762; PubMed=10524237;
RA Poudexer K., Nelson N., Dubose R.F., Black R.A., Cerretti D.P.;
RT "The identification of seven metalloproteinase-disintegrin (ADAM)
RT genes from genomic libraries.";
RN Gene 237:61-70(1999).
CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
CC CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=1; Synonyms=Epsilon;
CC IsoId=Q9P0K1-1; Sequence=Displayed;
CC Name=2; Synonyms=Delta;
CC IsoId=Q9P0K1-2; Sequence=VSP_005482, VSP_005484;
CC Name=3; Synonyms=Alpha;
CC IsoId=Q9P0K1-3; Sequence=VSP_005483;
CC Name=4; Synonyms=Beta;
CC IsoId=Q9P0K1-4; Sequence=VSP_005482, VSP_005483;
CC Name=5;
CC IsoId=Q9P0K1-5; Sequence=VSP_005482;
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. DETECTED SLIGHTLY
CC OR NOT AT ALL IN OTHER TISSUES.
CC -1- PTM: THE PRECURSOR IS CLEAVED BY A PURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF155382; AAF73289.1; -;
CC EMBL; AF155381; AAF73288.1; -;

DR EMBL; AB009671; BAA32349.1; -;
DR EMBL; AB009671; BAA32350.1; -;
DR EMBL; AF073291; AAF22476.2; -;
DR EMBL; AF158637; AAD55251.1; -;
DR HSRP; P18619; 1FVL;
DR MEROPS; M12.978; -;
DR MIM; 603709; -;
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005178; F:integral binding activity; NAS.
DR GO; GO:0007162; P:negative regulation of cell adhesion; NAS.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR002870; Pcp_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR006025; Zn_MTPeptide.
DR Pfam; PF01562; Pcp_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; D1SIN; 1.
DR PROSITE; PS50215; ADAM_MEROP; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
DR Signal; GlycoProtein; Transmembrane; EGF-like domain;
KW Alternative splicing.
FT SIGNAL 1 25
FT PROPEP 26 222
FT CHAIN 223 906
FT DOMAIN 223 736
FT TRANSMEM 737 757
FT DOMAIN 758 906
FT DOMAIN 223 438
FT DOMAIN 444 531
FT DOMAIN 532 678
FT DOMAIN 675 712
FT DISULFID 349 433
FT DISULFID 503 516
FT DISULFID 679 694
FT DISULFID 688 700
FT DISULFID 702 711
FT CARBOHYD 175 175
FT CARBOHYD 519 519
FT CARBOHYD 634 634
FT CARBOHYD 675 675
FT VARSPPLIC 768 803
FT /FTID=VSP_005482.
FT VARSPPLIC 860 906
FT /FTID=VSP_005483.
FT VARSPPLIC 859 859
FT /FTID=VSP_005484.
FT CONFLICT 81 81
FT SEQUENCE 906 AA; 100432 MW; 265ECCD0FAC088B CRC64;
SQ

Query Match 55.7%; Score 185; DB 1; Length 906;
Best Local Similarity 56.4%; Pred. No. 3e-12;
Matches 31; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 1 CSLNGAHCSGPGCCNNTSCLPFGPGYECRDVAVECDITTEYCTGDSGCPNPLHK 55
DB 477 CTLTGDSGCSGDLCK--KCKFGPGYTCRAVNDCCDIRTCGSGNSGCABNHHK 529

RESULT 5
AD22_MOUSE

ID AD22_MOUSE STANDARD: PRT: 857 AA.
 AC Q9RI6; Q9RI6; 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22).
 GN ADAM22.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Brain;
 RX MEDLINE=99365303; PubMed=10433968;
 RA Sagane K., Yamazaki K., Mizui Y., Tanaka I.;
 RT "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23";
 RL Gene 236:79-86(1999).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=Q9RI6-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9RI6-2; Sequence=VSP_005485;
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE BRAIN.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC -----
 CC EMBL; AB009674; BAA83382.1; -
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12.978: -
 DR MGD; MGI:1340046; Adam22.
 DR InterPro; IPR006586; ADAM_cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002870; PEP_M12B_propep.
 DR InterPro; IPR001590; Reptolyasin.
 DR InterPro; IPR006025; Zn_MTPepdase.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; Rep_M12B_propep; 1.
 DR Pfam; PF01421; Reptolyasin; 1.
 DR ProDom; PD000664; disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00500; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEROP; 1.
 DR PROSITE; PS50427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 DR PROSITE; PS00186; EGF_2; FALSE_NEG.
 KM Signal; Glycoprotein; Transmembrane; EGF-like domain;
 KM Alternative splicing.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 223 BY SIMILARITY.
 FT CHAIN 224 857 ADAM 22.
 FT DOMAIN 24 734 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 735 755 POTENTIAL.
 FT DOMAIN 756 857 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 224 436 METALLOPROTEINASE-LIKE.
 FT DOMAIN 442 529 DISINTEGRIN-LIKE.
 FT DOMAIN 533 666 CYS-RICH.
 FT DOMAIN 673 710 EGF-LIKE.
 FT DISULFID 347 431 BY SIMILARITY.
 FT DISULFID 501 514 POTENTIAL.
 FT DISULFID 677 692 BY SIMILARITY.
 FT DISULFID 686 698 BY SIMILARITY.
 FT DISULFID 700 709 BY SIMILARITY.
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 673 673 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 766 801 Missing (in isoform Beta).
 FT FT
 SO SEQUENCE 857 AA; 94740 MW; CB88FB7000208E09 CRC64;
 Query Match 55.4%; Score 184; DB 1; Length 857;
 Best Local Similarity 56.4%; Pred. No. 3,7e-12;
 Matches 31; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
 OY 1 CSLSNGAHGSDGPCNNNTSCLFQPRGYECRDVAVNCDITRYCTGDSGOCPPNHLK 55
 DB 475 CTLTQDSQSDGLCCCK--KCKFPLGTVCRAVANDCDIREICSGNSQCAPNVHK 527
 RESULT 6
 AD22_XENLA STANDARD: PRT: 935 AA.
 AC AD22_XENLA
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
 DE (Metalloproteinase-disintegrin domain 22) (MDC11.2).
 GN ADAM22 OR MDC11B.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenoportidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=99102794; PubMed=9882486;
 RA Cai H., Kraetzschmar J., Alfandari D., Hunnicutt G., Blobel C.P.;
 RT "Neural crest-specific and general expression of distinct
 RT metalloproteinase-disintegrins in early Xenopus laevis development";
 RL Dev. Biol. 204:508-524(1998).
 RN [2]
 RP SEQUENCE OF 464-511 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97349132; PubMed=9205136;
 RA Shilling F.M., Kraetzschmar J., Cai H., Weiskamp G., Gayko U.,
 RA Leibow J., Wyles D.G., Nuccitelli R., Blobel C.P.;
 RT "Identification of metalloproteinase/disintegrins in Xenopus laevis
 RT testis with a potential role in fertilization";
 RL Dev. Biol. 186:155-164(1997).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEINASE-LIKE PROTEIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: LOW LEVELS IN ADULT TISSUES. NOT DETECTED IN
 CC DEVELOPING EMBRYOS.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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[illegible]

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sciatic nerve;
RX MEDLINE=20556183; PubMed=1102971;
RA Bosse F., Pezold G., Greiner-Peter R., Pippiers U., Gillen C.,
RA Mueller H.-W.,
RT "Cellular localization of the disintegrin CRII-7/rMDC5 mRNA in rat
RT PNS and CNS and regulated expression in postnatal development and
RT after nerve injury."
RL Glia 32:313-327(2000).
CC -1- FUNCTION: May be involved in cell-surface proteolysis, cell
CC adhesion or intracellular protein maturation.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (Potential).
CC -1- SUBUNIT: Interacts with ITGA3-ITGB3 (vitronectin receptor),
CC PACSIN3 and SNX9. PACSIN3 and SNX9 preferentially bind the
CC precursor but not the processed form of ADAM15, suggesting that
CC the interaction occurs in a secretory pathway compartment prior to
CC the medial Golgi (By similarity). Interacts specifically with Src
CC family protein-tyrosine kinases (PTKs) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, SPINAL CORD,
CC SCIATIC NERVE AND LUNG. EXPRESSED AT LOWER LEVELS IN ALL OTHER
CC TISSUES. IN THE PERIPHERAL NERVOUS SYSTEM, EXPRESSED PREDOMINANTLY
CC BY SCHWANN CELLS. IN THE CENTRAL NERVOUS SYSTEM, PREFERENTIALLY
CC EXPRESSED BY NEURONAL CELLS.
CC -1- INDUCTION: IN RESPONSE TO SCIATIC NERVE INJURY.
CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
CC SORTING NEXTIN 9 (BY SIMILARITY).
CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA5V-BETA3 (BY
CC SIMILARITY).
CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FUTIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -1- PTM: Phosphorylation increases association with PTKs (By
CC similarity).
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 disintegrin domain.

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CC EMBL: AJ251198; CAB61762.1; -.
DR HSSP: P17494; IKST.
DR MEROPS: M12.215; -.
DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF_1like.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; RepPolysin.
DR InterPro: IPR006025; Zn_Mtpedease.
DR Pfam: PF00200; disintegrin.1.
DR Pfam: PF01562; Pep_M12B_propep.1.
DR Pfam: PF01421; RepPolysin.1.
DR ProDom: PD006664; Disintegrin.1.
DR SMART: SMO0608; ACR.1.
DR SMART: SMO050; DISTR.1.
DR PROSITE: PS50215; ADAM_MEPRO.1.
DR PROSITE: PS00427; DISINTEGRIN.1; FALSE_NEG.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00022; EGF.1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 1; FALSE_NEG.
DR PROSITE: PS00142; ZINC_PROTEASE.1.
DR PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.

KW Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
 KW Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
 FT SIGNAL 1 17
 FT PROPEP 18 208
 FT CHAIN 209 816
 FT DOMAIN 209 698
 FT TRANSMEM 699 719
 FT DOMAIN 720 816
 FT DOMAIN 209 416
 FT DOMAIN 423 510
 FT DOMAIN 511 658
 FT DOMAIN 659 687
 FT DOMAIN 700 713
 FT SITE 768 774
 FT SITE 803 809
 FT SITE 180 180
 FT METAL 350 350
 FT ACT_SITE 351 351
 FT METAL 354 354
 FT METAL 360 360
 FT DISULFID 325 411
 FT DISULFID 482 495
 FT DISULFID 659 669
 FT DISULFID 663 675
 FT DISULFID 677 686
 FT MOD_RES 717 717
 FT MOD_RES 737 737
 FT CARBOHYD 57 57
 FT CARBOHYD 239 239
 FT CARBOHYD 391 391
 FT CARBOHYD 394 394
 FT CARBOHYD 608 608
 FT CARBOHYD 613 613
 SQ SEQUENCE 816 AA; 88051 MW; B9D2CE023266FC27 CRC64;

Query Match 52.3%; Score 173.5; DB 1; Length 816;
 Best Local Similarity 53.7%; Pred. No. 4,4e-11;
 Matches 29; Conservative 8; Mismatches 14; Indels 3; Gaps 2;

QY 1 CSLSNGAHC-SDGPCNNTSCLPQPGVECDANVEDITEYCTGDSGCCPPNL 53
 DB 455 COLPFGACASDGGCCCN--CKLQPAQWQRLPTDCCDLPEFLCIDSQCPPDI 506

RESULT 8
 AD15_HUMAN STANDARD; PRT; 814 AA.
 AC Q13444; Q13493; Q96C78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADAM15 precursor (EC 3.4.24.-) (A disintegrin and metalloprotease domain 15) (Metalloprotease-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein) (Metargidin).
 GN ADAM15 OR MDC15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Breast carcinoma;
 RX MEDLINE=96214870; PubMed=8617717;
 RA Knaetzschmar J., Lum L., Blobel C.P.;
 RT "Metargidin, a membrane-anchored metalloprotease-disintegrin protein with an RGD integrin binding sequence.";
 RL J. Biol. Chem. 271:4593-4596(1996).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Umbilical vein;
 RX MEDLINE=97192141; PubMed=9039960;
 RA Herren B., Raines E.W., Ross R.;

RT "Expression of a disintegrin-like protein in cultured human vascular
 RT cells and in vivo.";
 RL FASEB J. 11:173-180(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Karkkainen I., Huovila A.-P.J.;
 RT "The characterization of human ADAM15 gene structure and promoter
 RT region.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Haen F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16099-16903(2002).
 RN [5]
 RP INTERACTION WITH INTEGRIN ALPHA-V-BETA3.
 RX MEDLINE=98194837; PubMed=9516430;
 RA Zhang X.P., Kamata T., Yokoyama K., Puzon-McLaughlin W., Takada Y.;
 RT "Specific interaction of the recombinant disintegrin-like domain of
 RT MDC-15 (metargidin, ADAM-15) with integrin alphavbeta3.";
 RL J. Biol. Chem. 273:7345-7350(1998).
 RN [6]
 RP PHOSPHORYLATION OF TYR-715 AND TYR-735.
 RX MEDLINE=21826475; PubMed=11741292;
 RA Poghosyan Z., Robbins S.M., Houslay M.D., Webster A., Murphy G.,
 RA Edwards D.R.;
 RT "Phosphorylation-dependent interactions between ADAM15 cytoplasmic
 RT domain and Src family protein-tyrosine kinases.";
 RL J. Biol. Chem. 277:4999-5007(2002).
 CC -1- FUNCTION: May be involved in cell-surface proteolysis, cell
 CC adhesion or intracellular protein maturation.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Interacts with ITGA5-ITGB3 (vitronectin receptor),
 CC PACSIN3 and SNX9. PACSIN3 and SNX9 preferentially bind the
 CC precursor but not the processed form of ADAM15, suggesting that
 CC the interaction occurs in a secretory pathway compartment prior to
 CC the medial Golgi (By similarity). Interacts specifically with Src
 CC family protein-tyrosine kinases (PTKs).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. OVEREXPRESSED IN
 CC ARTERIOSCLEROTIC LESIONS. CONSTITUTIVELY EXPRESSED IN CULTURED
 CC ENDOTHELIAL AND SMOOTH MUSCLE.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHLIN I AND
 CC SORTING NEXTIN 9 (BY SIMILARITY).
 CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA-V-BETA3.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FUIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- PTM: Phosphorylation increases association with PTKs.
 CC -1- SIMILARITY: Belongs to peptidase family M2B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----
 DR EMBL; U46005; AAC5112.1; -
 DR EMBL; U41767; AAC50404.1; -
 DR EMBL; AF314227; AA44189.1; -
 DR EMBL; BC014566; AA414566.1; -
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12.215; -
 DR Genew; HGNC:193; ADAM15.
 DR MIM; 605548; -
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR002870; Pep_M12B_propep.
 DR InterPro; IPR001590; Reprolysin.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SMO0050; ACR; 1.
 DR SMART; SMO0050; DISIN; 1.
 DR PROSITE; PS00215; ADAM_MERPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS00214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR Hydrolyase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
 DR Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
 FT SIGNAL 1 17
 FT PROPEP 18 206
 FT CHAIN 207 814
 FT DOMAIN 207 696
 FT TRANSMEM 697 717
 FT DOMAIN 718 814
 FT DOMAIN 207 814
 FT DOMAIN 421 508
 FT DOMAIN 509 656
 FT DOMAIN 657 685
 FT SITE 766 772
 FT SITE 801 807
 FT SITE 179 179
 FT SITE 484 486
 FT METAL 348 348
 FT ACT SITE 349 349
 FT METAL 352 352
 FT METAL 358 358
 FT DISULFID 323 409
 FT DISULFID 480 493
 FT DISULFID 657 667
 FT DISULFID 661 673
 FT DISULFID 675 684
 FT MOD_RES 715 715
 FT MOD_RES 735 735
 FT CARBOHYD 237 237
 FT CARBOHYD 389 389
 FT CARBOHYD 392 392
 FT CARBOHYD 606 606
 FT CARBOHYD 611 611
 FT CONFLICT 714 714
 FT CONFLICT 791 791
 FT SEQUENCE 814 AA; 87716 MW; 683A8368AD30996B CRC64;

Query Match 50.8%; Score 168.5; DB 1; Length 814;
 Best Local Similarity 51.9%; Pred. No. 1.5e-10;

Matches 28; Conservative 8; Mismatches 15; Indels 3; Gaps 2;
 QY 1 CSLNSGANC-SDGPCNNNTSCLFPQPRGECRDANVEDITEYCTGDSGCCPPL 53
 DB 453 COLRPAGCASCADPCCON--COLRPSGWCQPRTRGCDLPFCGDSGCCPPLV 504

RESULT 9
 AD30_HUMAN
 ID AD30_HUMAN STANDARD; PRT; 790 AA.
 AC Q9UKF2; Q9UKF1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 30 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 30).
 GN ADAM30.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Testis;
 RX MEDLINE=99443746; PubMed=10512762;
 RA Cerretti D.P., Dubose R.F., Black R.A., Nelson N.;
 RT "Isolation of two novel metalloproteinase-disintegrin (ADAM) cDNAs that show testis-specific gene expression.";
 RL Biochem. Biophys. Res. Commun. 263:810-815(1999).
 CC -1- FUNCTION: MAY BE INVOLVED IN SPERMATOGENESIS AND FERTILIZATION.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=Q9UKF2-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9UKF2-2; Sequence=VSP_005494;
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN TESTIS.
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
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DR EMBL; AF171933; AA03760.1; -
 DR EMBL; AF171933; AA03760.1; -
 DR HSSP; P02877; IHEV.
 DR MEROPS; M12.202; -
 DR Genew; HGNC:208; ADAM30.
 DR MIM; 604779; -
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR InterPro; IPR006586; ADAM_cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR002870; Pep_M12B_propep.
 DR InterPro; IPR001590; Reprolysin.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SMO0050; ACR; 1.
 DR SMART; SMO0050; DISIN; 1.


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DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR006025; Zn_MTPeptide.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Hydrolase; Metalloprotease; zinc; Signal; Glycoprotein; Zymogen;
KW Transmembrane; EGF-like domain; Alternative splicing.
FT SIGNAL 1 29
FT PROPEP 30 203
FT CHAIN 204 813
FT DOMAIN 30 701
FT TRANSMEM 702 722
FT DOMAIN 723 813
FT DOMAIN 204 409
FT DOMAIN 417 502
FT DOMAIN 503 648
FT DOMAIN 649 681
FT SITE 133 133
FT METAL 345 345
FT ACT_SITE 346 346
FT METAL 349 349
FT METAL 355 355
FT DISULFID 360 404
FT DISULFID 360 388
FT DISULFID 475 488
FT DISULFID 653 663
FT DISULFID 657 669
FT DISULFID 671 680
FT CARBOHYD 109 109
FT CARBOHYD 145 145
FT CARBOHYD 231 231
FT CARBOHYD 276 276
FT CARBOHYD 448 448
FT VARSPLIC 636 661
SQ SEQUENCE 813 AA; 87738 MW; 90713A95668D5569 CRC64;

Query Match 48.2%; Score 160; DB 1; Length 813;
Best Local Similarity 48.1%; Pred. No. 1.le-09;
Matches 26; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 CSLNSGAHCSDPCCNNTSCLPFRGYECRDVNECDITEYCTGDSGQCPNLIH 54
DB 449 CSLRPGAQCAHGDCC--VRCLLKPAGALCRQAMGDCDDLPEFCTGTSSHCPDVI 500

```

Search completed: October 21, 2003, 10:06:25
Job time : 10.6855 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:53:36 ; Search time 38.3962 Seconds
(without alignments)
369.643 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586

Perfect score: 332
Sequence: 1 CSLNGAHCHSDGPCNNNTSC.....CDITEYCTGDSGQCPPMLHK 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mmc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacterioph: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	100.0	832	4	075077 homo sapien
2	319	96.1	690	11	08CCJ3 mus musculu
3	319	96.1	829	11	09RIV7 mus musculu
4	173.5	52.3	81	11	P97778 ratu
5	168.5	50.8	814	4	096C78 mus sapien
6	168	50.6	617	13	090499 echis pyram
7	167	50.3	790	4	08TR27 homo sapien
8	165	49.7	836	6	019057 pongo pygma
9	162	48.8	694	5	09G215 drosophila
10	162	48.8	1182	4	09VXL1 drosophila
11	160	48.2	812	4	08N0W6 mus sapien
12	158.5	47.7	809	11	08CA82 mus musculu
13	158.5	47.7	864	11	08C720 mus musculu
14	154.5	46.5	812	6	077779 bos taurus
15	153	46.1	736	6	028482 macaca fasc
16	150	45.2	873	13	042595 xenopus lae

17	149.5	45.0	212	13	090Y44 agkistrodon
18	149.5	45.0	610	13	09Y120 agkistrodon
19	149	44.9	914	13	012960 xenopus lae
20	148	44.6	791	11	060813 mus musculu
21	148	44.6	804	11	060410 cavia porce
22	147	44.3	451	13	09PT49 atractaspis
23	146.5	44.1	609	13	09W6M5 agkistrodon
24	146	44.0	792	6	019061 saguinus oe
25	146	44.0	922	13	08UVE2 coturnix co
26	146	44.0	822	13	090282 crocalus at
27	145.5	43.8	610	13	093523 boctrops ja
28	145.5	43.8	610	13	093523 boctrops ja
29	145.5	43.8	610	13	093523 boctrops ja
30	145	43.7	789	11	P70505 ratu
31	144.5	43.5	587	5	08T319 drosophila
32	144.5	43.5	959	5	09VPR0 drosophila
33	144	43.4	825	6	046552 papio anubi
34	144	43.4	825	6	028477 macaca fasc
35	144	43.4	838	6	019056 papio anubi
36	144	43.4	905	6	028476 macaca fasc
37	143	43.1	620	13	042138 agkistrodon
38	143	43.1	702	11	08BMR5 mus musculu
39	143	43.1	714	11	08K4K0 mus musculu
40	141	42.5	797	11	08R465 mus musculu
41	141	42.5	797	11	08R5G5 mus musculu
42	140.5	42.3	190	13	093518 agkistrodon
43	140	42.2	697	11	08BMR4 mus musculu
44	139.5	42.0	761	11	08CDV3 mus musculu
45	139	41.9	845	11	061072 mus musculu

ALIGNMENTS

RESULT 1
ID 075077 PRELIMINARY; PRT; 832 AA.
AC 075077;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MDC3 (ADAM22 protein).
GN ADAM22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98359734; PubMed=9693107;
RA Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;
RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
and MDC3: novel human cellular disintegrins highly expressed in the
brain.";
RL Biochem. J. 334:93-98(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA "Identification and characterization of ADAM 22, a novel
RT metalloproteinase/disintegrin protein.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009672; BAA32351.1; -;
DR EMBL; AJ005580; CAC20365.1; -;
DR HSSP; P18619; IFVL.
DR MEROPS; M2.979; -;
DR Genew; HGNC:202; ADAM23.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; Pep_M12B_propep.

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DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin. 1.
DR Pfam; PF01562; Pep_M12B_propep. 1.
DR Pfam; PF01421; Reprolysin. 1.
DR ProDom; PD000664; Disintegrin. 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 832 AA; 91923 MW; 78419670E1C24EF CRC64;

Query Match
Best Local Similarity 100.0%; Score 332; DB 4; Length 832;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 532 CSLSNAGHCSGDPCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 586

RESULT 2
Q8CC33 PRELIMINARY; PRT; 690 AA.
AC Q8CC33;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE A disintegrin and metalloprotease domain 23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=dienecephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL EMBL; AK034022; BAC28550.1;
SQ SEQUENCE 690 AA; 77228 MW; B61699141A6CA6A6 CRC64;

Query Match
Best Local Similarity 96.4%; Score 319; DB 11; Length 690;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 529 CSLSNAGHCSGDPCCNNTSCLFQSRGYECRDVAVNSCDITEYCTGDSGCCPPNLHK 583

RESULT 3
Q9R1V7 PRELIMINARY; PRT; 829 AA.
AC Q9R1V7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADAM23.
GN ADAM23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99365303; PubMed=10433968;
RX Segane K., Yamazaki K., Mizui Y., Tanaka I.;
```

```
RT "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23.";
RL Gene 236:79-86(1999).
RL EMBL; AB009673; BAAB3381.1; -
DR HSSB; P18619; 1FVL.
DR MEROPS; M12.979; -.
DR MGD; MGI:1345162; Adam23.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin. 1.
DR Pfam; PF01562; Pep_M12B_propep. 1.
DR Pfam; PF01421; Reprolysin. 1.
DR ProDom; PD000664; Disintegrin. 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 829 AA; 91547 MW; FE6BCD69DD50F53A CRC64;

Query Match
Best Local Similarity 96.1%; Score 319; DB 11; Length 829;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 529 CSLSNAGHCSGDPCCNNTSCLFQSRGYECRDVAVNSCDITEYCTGDSGCCPPNLHK 583

RESULT 4
P97778 PRELIMINARY; PRT; 81 AA.
ID P97778;
AC P97778;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TMDC VI (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley; TISSUE=Testis;
RX MEDLINE=97436783; PubMed=9291465;
RA Freyne J., Jury J.A., Barker H.L., Hall L.;
RT "Sequence analysis, tissue distribution, and expression in prepubertal
RT and adult rat testis."
RL Mol. Reprod. Dev. 48:159-167(1997).
RL EMBL; Y11492; CAA72278.1; -.
DR HSSB; P17494; 1KST.
DR MEROPS; M12.215; -.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; disintegrin. 1.
DR ProDom; PD000664; Disintegrin. 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 8622 MW; 104013827E1096CB CRC64;

Query Match
Best Local Similarity 52.3%; Score 173.5; DB 11; Length 81;
Matches 29; Conservative 8; Mismatches 14; Indels 3; Gaps 2;

QY 1 CSLSNAGHCSGDPCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 53
DB 16 COLRRGACASDGPCCCN--CKLPAGQCRLPTDDCDLPFCUCGDSGCCPPDI 67
```

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RESULT 5
096C78 PRELIMINARY; PRT; 814 AA.
AC 096C78
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE A disintegrin and metalloproteinase domain 15 (metargidin)
DE (Metalloprotease disintegrin).
GN ADAM15.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Karkkainen I., Huovila A.-P.J.;
RT "The characterization of human ADAM15 gene structure and promoter
region."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014566; AAH14566.1; -.
DR EMBL; AF114227; AAH4189.1; -.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR006025; Zn_MTPpeptidase.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR PROSITE; PSS0215; ADAM_MERPRO; 1.
DR PROSITE; PSS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS00186; EGF_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Intergrin; Protease.
SQ SEQUENCE 814 AA; 8717 MW; 683A8368AD3096B CRC64;

Query Match 50.8%; Score 168.5; DB 4; Length 814;
Best Local Similarity 51.9%; Pred. No. 2.2e-14;
Matches 28; Conservative 8; Mismatches 15; Indels 3; Gaps 2;

OY 1 CSLSNGAHC-SDGFCNNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPNTL 53
Db 453 CQLRPGAGCAGSDGFCGCGN--CQLRPSGWCGRPTRGDDCLPFCFGDSGDCPPDV 504

RESULT 6
090499 PRELIMINARY; PRT; 617 AA.
AC 090499;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Metalloprotease.
GN ECHI.
OS Echinodermata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=8700;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=95010025; PubMed=7925363;
RA Paine M.V.I., Moura-Da-Silva A.M., Theakston R.D.G., Crampton J.M.;
"Cloning of metalloprotease genes in the carpet viper (Echis pyramidum
```

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RT (leakey): Further members of the metalloprotease/disintegrin gene
family."
RL Eur. J. Biochem. 224:483-486(1994).
DR EMBL; X78970; CA55565.1; -.
DR HSP; P18619; 1FVL.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR006025; Zn_MTPpeptidase.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PSS0215; ADAM_MERPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PSS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Protease.
KW CHAIN 193 617 METALLOPROTEASE.
SQ SEQUENCE 617 AA; 69310 MW; 83DC3DA5F4F3AFBA CRC64;

Query Match 50.6%; Score 168; DB 13; Length 617;
Best Local Similarity 52.0%; Pred. No. 1.9e-14;
Matches 26; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

OY 1 CSLSNGAHCSDGFCNNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCP 50
Db 436 CKLTPSGCAGDGCN--CQFRFPARTCRKIDCDVPEYCTGSGGCEP 483

RESULT 7
08TB27 PRELIMINARY; PRT; 790 AA.
AC 08TB27;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE A disintegrin and metalloproteinase domain 30.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028372; AAH28372.1; -.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PSS0215; ADAM_MERPRO; 1.
DR PROSITE; PSS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS00186; EGF_2; 1.
DR Intergrin.
SQ SEQUENCE 790 AA; 88940 MW; 42EC8A5F66ECCDA3 CRC64;

Query Match 50.3%; Score 167; DB 4; Length 790;
Best Local Similarity 50.9%; Pred. No. 3.4e-14;
Matches 28; Conservative 9; Mismatches 16; Indels 2; Gaps 1;
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Oy 1 CSLSNGAHCSGDPCCNNNTSCLEFQPRGYECRDVAVECDITETCTGDSGCCPPNLRK 55
DB 431 CKLQAGANCSTIGLCCHD--CRFRPSGYVCROGRGNCODLAIEYCDGSSSCPNVYK 483

RESULT 8
ID 019057 PRELIMINARY; PRT; 836 AA.
AC 019057;
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Fertilin alpha protein.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98376167; PubMed=9712322;
RA Juy J.A., Frayne J., Hall L.;
RT "Sequence analysis of a variety of primate fertilin alpha genes:
RT Evidence for non-functional genes in the gorilla and man.";
RL Mol. Reprod. Dev. 51:92-97(1998).
DR EMBL; Y15491; CAA75659.1; -.
DR HSSP; P18619; 1FVL.
DR MEROPS; M12_201; -.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Reprolysin.
DR InterPro; IPR006025; Zn_MTPeptidase.
DR Pfam; PF00200; disintegrin_1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERPO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 836 AA; 93135 MW; 659CDE6A5991BA12 CRC64;

Query Match 49.7%; Score 165; DB 6; Length 836;
Best Local Similarity 50.9%; Pred. No. 6.8e-14;
Matches 28; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

Oy 1 CSLSNGAHCSGDPCCNNNTSCLEFQPRGYECRDVAVECDITETCTGDSGCCPPNLRK 55
DB 473 CILKAKACSDGDPCH--KCKFQRKGYPGRPSRSCDLPFCNGTSALCPDRHRK 525

RESULT 9
ID 09GZ15 PRELIMINARY; PRT; 694 AA.
AC 09GZ15;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MIND-WELD (Fragment).
GN MMD OR CG9163 OR CG15603 OR CG15604.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Harper C.H., Chase B.A.;
RT "The Drosophila mind-weld gene encodes a neuronally expressed ADAM
RT protein.";
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
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DR EMBL; AF252287; AAF98331.1; -.
DR HSSP; P18619; 1FVL.
DR FlyBase; FBgn0041109; mmd.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; pep_M12B_propep.
DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin_1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERPO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW EGF-1like domain.
FT NON-TER 1
SQ SEQUENCE 694 AA; 76317 MW; 37736F7B064A72E9 CRC64;

Query Match 48.8%; Score 162; DB 5; Length 694;
Best Local Similarity 47.3%; Pred. No. 1.4e-13;
Matches 26; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

Oy 1 CSLSNGAHCSGDPCCNNNTSCLEFQPRGYECRDVAVECDITETCTGDSGCCPPNLRK 55
DB 369 CKLSEAGCAGACCD--QCLRLRPKDYICRSNNECDLPEVCDEIGCGCPEDVYK 421

RESULT 10
ID 09VXL1 PRELIMINARY; PRT; 1182 AA.
AC 09VXL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG9163 protein.
GN MMD OR CG9163 OR CG15603 OR CG15604.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkelley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chample W., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abtil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baou A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Beus P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butts K.C., Busam D.A., Butler H., Cadeau E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Laeko P., lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).

[12] SEQUENCE FROM N.A.

RA Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorselt V., Doup L.E., Doyle C., Dresnek D., Fafan D.,
 RA Ferriera S., Frise E., Galle R.F., Gary N.S., George H.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Iobegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[13] SEQUENCE FROM N.A.

RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hrdecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Ceiniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[14] SEQUENCE FROM N.A.

RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[15] SEQUENCE FROM N.A.

RA FlyBase; submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE003500; AAF48548.2; -.
 DR HSSP; P18619; 1FVL.
 DR FlyBase; FBgn0041109; mmd.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001590; Reptolysin.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01421; Reptolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR PRODOM; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPRO; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 SQ SEQUENCE 1182 AA; 128515 MW; F58BA6E349C2ECA9 CRC64;

Query Match 48.8%; Score 162; DB 5; Length 1182;
 Best Local Similarity 47.3%; Pred. No. 2,5e-13;
 Matches 26; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

Oy 1 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGQCPPLHK 55
 Db 231 CKLSEACASGACCD--QCLAPKDYICRDSNNECDLPYCGEIGCCSDVFK 283

Search completed: October 21, 2003, 10:10:36
 Job time : 40.3962 secs

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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:12:31 ; Search time 3432.65 Seconds
(without alignment)
1239.449 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599
Perfect score: 630
Sequence: 1 PTKLFEPTECGNGYVEAGEE.....CPMLHKQD/ACNONGRC 104

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xjh
-Q=/cgr2_1/USPRO.spool/US09634252/runat_21102003_090323_3370/app_query.fasta_1.462
-DB=GenBdb1 -QPM=faetap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOCPLC=0 -LOOPEXT=0
-UNITS=b1bs -START=1 -END=-1 -MATRIX=b1osum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=10 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09634252 @CGN 1.1 3608 @runat_21102003_090323_3370 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGCLOS
-DEV_TIMEOUT=10 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenBdb1:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_ey:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vtc:*
38: em_ey:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	2499	6 BD130423	BD130423 DNs and
2	630	100.0	3054	6 E26532	E26532 Novel prote
3	630	100.0	3054	9 AB009672	AB009672 Homo sapi
4	630	100.0	3079	9 HSAS580	AJ005580 Homo sapi
5	630	100.0	4043	6 AX299710	AX299710 Sequence
6	611	97.0	2891	6 AB009673	AB009673 Mus muscu
7	586	93.0	1668	6 AX235014	AX235014 Sequence
8	404.5	64.2	1464	6 E10490	E10490 CDNA encodi
9	404.5	64.2	1464	6 E125845	E125845 Sequence 5
10	404.5	64.2	1464	6 E13482	E13482 Sequence 5
11	404.5	64.2	2908	6 HDMDC	D17380 Homo sapien
12	404.5	64.2	2913	6 E10492	E10492 CDNA encodi
13	404.5	64.2	2913	6 E125847	E125847 Sequence 7
14	404.5	64.2	2913	6 E13484	E13484 Sequence 7
15	404.5	64.2	2923	6 E10491	E10491 CDNA encodi
16	404.5	64.2	2923	6 E125846	E125846 Sequence 6
17	404.5	64.2	2923	6 E13483	E13483 Sequence 6
18	404.5	64.2	3168	6 AB009675	AB009675 Homo sapi
19	404.5	64.2	3183	6 E10493	E10493 CDNA encodi
20	404.5	64.2	3183	6 E125848	E125848 Sequence 8
21	404.5	64.2	3183	6 E13485	E13485 Sequence 8
22	404.5	64.2	3229	10 AB009676	AB009676 Mus muscu
23	375	59.5	1588	5 AF032384	AF032384 Xenopus 1
24	364.5	57.9	2773	10 AB009674	AB009674 Mus muscu
25	363.5	57.7	2604	6 BD130424	BD130424 DNs and
26	363.5	57.7	2697	6 E26531	E26531 Novel prote
27	363.5	57.7	2786	9 AB009671	AB009671 Homo sapi
28	363.5	57.7	2796	9 AF155381	AF155381 Homo sapi
29	363.5	57.7	2805	6 E26530	E26530 Novel prote
30	363.5	57.7	2858	9 AF155382	AF155382 Homo sapi
31	363.5	57.7	3259	9 AF158637	AF158637 Homo sapi
32	363.5	57.7	3295	9 AF073291	AF073291 Homo sapi
33	357.5	56.7	3447	5 AF032383	AF032383 Xenopus 1
34	338.5	53.7	1674	6 AX235012	AX235012 Sequence
35	292	46.3	2541	9 AB055891	AB055891 Homo sapi
36	292	46.3	2642	6 AX686216	AX686216 Sequence
37	292	46.3	2649	6 AX319859	AX319859 Sequence
38	292	46.3	2705	6 AX686214	AX686214 Sequence
39	292	46.3	2762	6 AX686212	AX686212 Sequence
40	292	46.3	3033	6 HSM601104	AL117415 Homo sapi
41	292	46.3	3431	6 AR219232	AR219232 Sequence
42	292	46.3	3431	6 AX082151	AX082151 Sequence
43	292	46.3	3468	6 AR219233	AR219233 Sequence
44	292	46.3	3468	6 AX082153	AX082153 Sequence
45	292	46.3	3509	6 AX326807	AX326807 Sequence

RESULT 1

ALIGNMENTS

BD130423 2499 bp DNA linear PAT 18-SEP-2002
 LOCUS E26532
 DEFINITION DNAS and polypeptides of metalloprotease disintegrins SVP3-13 and SVP3-17.
 ACCESSION BD130423
 VERSION BD130423.1 GI:23225368
 KEYWORDS JP 2002503472-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Cerebetti, D.P.
 1 (bases 1 to 2499)
 DNAS and polypeptides of metalloprotease disintegrins SVP3-13 and SVP3-17
 Parent: JP 2002503472-A 2 05-FEB-2002;
 IMMUNEX CORP
 OS Homo sapiens (human)
 PN JP 2002503472-A/2
 PD 05-FEB-2002
 PR 11-FEB-1999 JP 2000531569
 PR 11-FEB-1998 US 60/074310
 PI DOUGLAS PAT CERRETTI
 PC C12N15/09, C07K16/40, C12N1/19, C12N1/21, C12N5/10, C12N9/64 PC
 C12Q1/37, G01N33/68,
 CC C12N15/00, C12N5/00
 CC DNAS and polypeptides of metalloprotease disintegrins CC
 SVP3-13 and SVP3-17
 FH Key
 FT source
 FT Location/Qualifiers
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BASE COUNT 677 a 593 c 645 g 584 t
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Alignment Scores:
 Pred. No.: 3 41e-56 Length: 2499
 Score: 630.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x BD130423 (1-2499)

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 Db 1466 CCAACAAAGCTATTGAGCCCAAGGATGTGGAATGATAGTGGAACCTGGGAGAG 1545
 QY 21 CysAaPcYsGlyPheHisValGluCyStYrGlyLeuCySylsYsCySerLeuSer 40
 Db 1546 TGTGATTGTGGTTTCATGTCGAAATGCTATGATTAATCTGTAAGAAATGTTCCCTCC 1605
 QY 41 AsnGlyAlaHisCySerAspGlyProCySAsaAsnThSerCysLeuPheGlnPro 60
 Db 1606 AACGGGGCTCACTGCAGCCAGCGGCCCTGCTGAACAATACCTCATGCTTTTTCAGCCA 1665
 QY 61 ArgGlyTYrGluCyArGAspAlaValAsnGluCyAspIleThrGluTYrCyStHrgly 80
 Db 1666 CGAGGGTATGATGCGGGATGCTGTGAACGAGTGTGATTAATCTGAAATTTGTACTGGA 1725
 QY 81 AspSerGlyGlnCySProAsnLeuHisIlysgInAspGlyTYrAlaCysAsnGlnAsn 100
 Db 1726 GACTCTGCTAGTGCACCAATCTTCTAATAGCAAGAGATATGCATGCAATCAAAAT 1785
 QY 101 GlnGlyArGcYs 104
 Db 1786 CAGGGCCGCTGC 1797

RESULT 2
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 LOCUS E26532
 DEFINITION Novel protein belonging to MDC gene family and DNA encoding the same.
 ACCESSION E26532
 VERSION E26532.1 GI:13026199
 KEYWORDS JP 1999155574-A/3.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Koji, S.
 1 (bases 1 to 3054)
 Novel protein belonging to MDC gene family and DNA encoding the same
 Patent: JP 1999155574-A 3 15-JUN-1999;
 EISAI CO LTD
 OS Homo sapiens (human)
 PN JP 1999155574-A/3
 PD 15-JUN-1999
 PR 01-DEC-1997 JP 1997330020
 PR KOJI SONE
 PI C12N15/09, C07K14/47, C07K16/18, C12N1/21, C12P21/02, C12Q1/68// PC
 (C12N15/09, C12R1/91), (C12N1/21, C12R1/19), (C12P21/02, C12R1/19), PC
 C12N15/00,
 CC C12N15/00, C12R1/91)
 CC Strandedness: Double;
 CC Topology: linear;
 FH Key
 FT CDS
 FT Location/Qualifiers
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 /organism="Homo sapiens"
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BASE COUNT 815 a 754 c 803 g 682 t
 ORIGIN

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 Pred. No.: 4 21e-56 Length: 3054
 Score: 630.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x E26532 (1-3054)

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 QY 61 ArgGlyTYrGluCyArGAspAlaValAsnGluCyAspIleThrGluTYrCyStHrgly 80
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 QY 81 AspSerGlyGlnCySProAsnLeuHisIlysgInAspGlyTYrAlaCysAsnGlnAsn 100
 Db 1949 GACTCTGCTAGTGCACCAATCTTCTAATAGCAAGAGATATGCATGCAATCAAAAT 2008
 QY 101 GlnGlyArGcYs 104
 Db 2009 CAGGGCCGCTGC 2020

RESULT 3
 LOCUS AB009672 3054 bp mRNA linear PRI 15-AUG-1998
 DEFINITION Homo sapiens mRNA for MDC3, complete cds.
 ACCESSION AB009672
 VERSION AB009672.1 GI:3419877
 KEYWORDS MDC3.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Sagan, K., Ohya, Y., Hasegawa, Y. and Tanaka, I.
 TITLE Metalloproteinase-like, disintegrin-like, cysteine-rich proteins
 MDC2 and MDC3: novel human cellular disintegrins highly expressed
 in the brain
 JOURNAL Biochem. J. 334 (Pt 1), 93-98 (1998)
 MEDLINE 98359734
 PUBMED 9693107
 REFERENCE 2 (bases 1 to 3054)
 AUTHORS Sagan, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-1997) Koji Sagan, Eisai Co., Ltd., Tsukuba
 Research Laboratories, Tokodai 5-1-3, Tsukuba, Ibaraki 300-2635,
 Japan (E-mail:k1-sagan@eisai.co.jp, Tel:+81-298-47-5813,
 Fax:+81-298-47-5367)
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 BASE COUNT 815 a 754 c 803 g 682 t
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 Score: 630.00 Matches: 104
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 Db 1769 TGTGATTGTGTTCATGTGGAATGCTATGAGATTATGCTGTAAAGAAATGTTCCCTCTCC 1828

QY 41 AenglyAlahisCyseSeraspGlyProCyseAsnAsnThrSerCyseuPhegiuPro 60
 Db 1829 AACGGGGCTCACTGACGACGACGGCCCTCTCTTAACAATACCTCAATGCTTTTTCAGCA 1888
 QY 61 ArgGlyTYrGluCyseArgAspAlaValaAengluCyseAspIleThrGluTYrCysthGly 80
 Db 1889 CGAGGGTATGATATGCGCGGATCTGTGAACGAGTGTGATTAATGATAATATTGATCGGA 1948
 QY 81 AspSerGlyGluCyseProProAsnleuHslYsGlnAspGlyTyValaCyseAengluPro 100
 Db 1949 GACTCTGGTCAGTGGCCACCAAACTTCTATAGCAAGACGAGATATGATCAATCAAAAT 2008
 QY 101 GlnGlyArgCys 104
 Db 2009 CAGGCGCGCTGC 2020
 RESULT 4
 LOCUS HSAS580 3079 bp mRNA linear PRI 18-JAN-2001
 DEFINITION Homo sapiens mRNA for adam23 protein.
 ACCESSION AJ005580
 VERSION AJ005580.1 GI:12053562
 KEYWORDS adam23 gene; Adam23 protein; disintegrin; metalloprotease.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Cal, S. and Lopez-Otin, C.
 TITLE Identification and characterization of ADAM 23, a novel
 metalloprotease/disintegrin protein
 JOURNAL Unpublished
 AUTHORS Lopez-Otin, C.
 TITLE Direct Submission
 JOURNAL Submitted (15-APR-1998) Lopez-Otin C., Biología y Biología
 Molecular, Universidad de Oviedo, C/ Julian Claveria 6, Oviedo,
 Asturias, 33006, SPAIN
 revised by author 23-APR-1998, revised by author 26-OCT-1998
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 Alignment Scores:
 Pred. No.: 4,256-56 Length: 3079
 Score: 630.00 Matches: 104
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
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 QY 41 AenglylAhlhScySerAspGlyProCysCysAsnAntHrSerCysleupheglupro 60
 DB 1658 AACGGGCTCACTGACGAGCGAGCGGCCCTGCTGTAACAATACCTCATGTTTTTACGCCA 1717
 QY 61 ArgglyTyrgluCysArgAspAlaValAsngluCysAspIleThrGluTyrcyThrgly 80
 DB 1718 CGAGGATATGATATCGCGGATCTGTGAACGAGTGTGATTAATGATTAATGATTAATGATTA 1777
 QY 81 AspserglyglncysProProAsnleuHlslysglnAspGlyTyraAlaCysAsnglnAsn 100
 DB 1778 GACTCTGGTCACTGCCACCAAAATCTTCAATAGCAAGCGATATGATCAATCAAAAT 1837
 QY 101 GlnGlyArgCys 104
 DB 1838 CAGGGCCCTGCTC 1849
 RESULT 5 4043 bp DNA linear PAT 26-NOV-2001
 LOCUS AX299710
 DEFINITION Sequence 2 from Patent WO0174857.
 ACCESSION AX299710.1 GI:1129252
 VERSION AX299710.1 GI:1129252
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Lopez-Otin,C., Freilij,J.M., Bianchi,A.B., Miguel,S.C., Garcia,J.M.
 and Trall,P.
 TITLE Methods and compositions for modulating integrin-mediated cell-cell
 interactions
 JOURNAL Patent: WO 0174857-A 2 11-OCT-2001;
 Bristol-Myers Squibb Co. (US)
 FEATURES
 source 1..4043
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 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-634-252a-4_COPY_496_599 (1-104) x AX299710 (1-4043)

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 DB 2742 GACTCTGGTCACTGCCACCAAAATCTTCAATAGCAAGCGATATGATCAATCAAAAT 2801
 QY 101 GlnGlyArgCys 104
 DB 2802 CAGGGCCCTGCTC 2813
 RESULT 6 2891 bp mRNA linear ROD 17-AUG-1999
 LOCUS AB009673
 DEFINITION Mus musculus mRNA for ADAM23, complete cds.
 ACCESSION AB009673.1 GI:5736618
 VERSION AB009673.1 GI:5736618
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (sites)
 AUTHORS Sagane,K., Yamazaki,K., Mizui,Y. and Tanaka,I.
 TITLE Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23
 JOURNAL Gene 236 (1), 79-86 (1999)
 MEDLINE 99365303
 PUBMED 10433368
 REFERENCE 2 (bases 1 to 2891)
 AUTHORS Sagane,K.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-1997) Koji Sagane, Eisai Co., Ltd., Tsukuba
 Research Laboratories, Tokodai 5-1-3, Tsukuba, Ibaraki 300-2635,
 Japan (E-mail:k-sagane@hsc.eisai.co.jp, Tel:+81-298-47-5613,
 Fax:+81-298-47-5367)
 COMMENT Sequence updated (07-Aug-1999).
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BASE COUNT 763 a 747 c 763 g 618 t
ORIGIN

Alignment Scores:
Pred. No.: 3.84e-54 Length: 2891
Score: 611.00 Matches: 100
Percent Similarity: 98.08% Conservative: 2
Best Local Similarity: 96.15% Mismatches: 2
Query Match: 96.98% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AB009673 (1-2891)

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Db 1736 CGAGGGATGATATGTCGGGATGCGGTAAACAGCTGATATCACCGAGTACTGACCTGGA 1795
QY 81 AspSerGlyGlnCysProProAsnLeuHisGlyGlnAspGlyTyrAlaCysAsnGlnAsn 100
Db 1796 GACTCTGGCCAGTGGCCACCGAACCTCATTAACAAAGATGCTATGCTCAATCAAAAT 1855
QY 101 GlnGlyArgCys 104
Db 1856 CAGGCTGCTGC 1867

RESULT 7
AX235014 1668 bp DNA linear PAT 11-SEP-2001
LOCUS
DEFINITION Sequence 17 from Patent WO0162905.
ACCESSION AX235014
VERSION AX235014.1 GI:15593673
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS Fenslow, W.C., Cerretti, D.P., Poindexter, K.M. and Black, R.A.
TITLE Integrin antagonists
JOURNAL Patent: WO 0162905-A 17 30-AUG-2001;
IMMUNEX CORPORATION (US)

FEATURES
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1. 1668
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LEPPKXKDTLSRTEVTVVVDVSHBEPVFMVYGVNHNKATKPREQVNST
YRVSVTLVHODMLNGKEYCKSVSKALPAPEKTSIAKQGPPEVQYTLPPSDE
LRKQVSLTCLVKGFPSPSDIAVEMESNNGPENNYKTPPVLDSDGSFLYSKLTIVKS
RMQGVNPFSCSVNHEALNHNHYOKSLSPSK"

Alignment Scores:
Pred. No.: 8.8e-52 Length: 1668
Score: 586.00 Matches: 96
Percent Similarity: 98.97% Conservative: 0
Best Local Similarity: 98.97% Mismatches: 1
Query Match: 93.02% Indels: 0
DB: 6 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AX235014 (1-1668)

QY 8 ThrGluCysGlyAsnGlyTyrValGluAlaGlyGluCysAspCysGlyPheHisVal 27
Db 85 ACTAGTTGTGGAATGATGATCGTCAAGCTGGGAGAGAGTGTATGTGTTTCATGTG 144
QY 28 GluCysTyrGlyLeuGlyCysGlyGlySerLeuSerAsnGlyAlaHisCysSerAsp 47
Db 145 GAATGCTATGATGATGCTGTAGAAATGTTCCCTCCAAACGGGCTCACTCAGCAG 204
QY 48 GlyProCysGlySerAsnSerCysLeuPheGluProArgGlyTyrGluCysArgAsp 67
Db 205 GGGCCCTGCTGTAACAATACCTCATGCTTTTTCACCCAGAGGATGATGATCCGGAT 264
QY 68 AlaValAsnGluCysAspIleThrGluTyrCysThrGlyAspSerGlyGlnCysProPro 87
Db 265 GCTGTGACAGAGTGTATATTAATGTAATTTGACTGAGAGACTGTGTCAGTCCACCA 324
QY 88 AsnLeuHisGlyGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCys 104
Db 325 AATCTTCATTAACAGACGATGATGATGATGATGATGATGATGATGATGATGATG 375

RESULT 8
E10490 1464 bp RNA linear PAT 29-SEP-1997
LOCUS
DEFINITION cDNA encoding a consensus region of MDC protein.
ACCESSION E10490
VERSION E10490.1 GI:22027323
KEYWORDS
SOURCE JP 1995330799-A/1.
Homo sapiens (human)
ORGANISM
Homo sapiens
Homo sapiens

REFERENCE
AUTHORS Nakamura, Y. and Emi, M.
TITLE MDC PROTEIN AND DNA CODING THE SAME
JOURNAL Patent: JP 1995330799-A 1 19-DEC-1995;
JAPAN FOUND CANCER RES, EISAI CO LTD
OS Homo sapiens (human)
PN JP 1995330799-A/1
PD 19-DEC-1995
PF 22-APR-1994 JP 1994084470
PR 14-MAY-1993 JP 93P 136602, 22-SEP-1993 JP 93P 257455, PR
23-FEB-1994 JP 94P 49904, 12-APR-1994 JP 94P 73328 PI
NKAHURA YUSUKE, EMI MITSURU
PC C07K16/32, C07K14/82, C12N1/21, C12N15/02, C12N15/09, C12P21/02, PC
C12P21/08
PC C1201/68, C01N33/53, C01N33/574, (C12N1/21, C12R1/19), (C12N15/09,
PC C12R1/91),
PC (C12P21/02, C12R1/19), (C12P21/08, C12R1/91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers

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FT      /organism='Homo sapiens'
FT      /tissue_type='Cerebellum'
FT      CDS          <1..>1464
FT                  /product='MDC protein'
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    1. 1464
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    /mol_type='genomic RNA'
    /db_xref='taxon:9606'
BASE COUNT      294 a      445 c      473 g      252 t
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Best Local Similarity: 65.42%      Mismatches: 23
Query Match:    64.21%      Indels:      5
DB:             Gaps:      2
US-09-634-252A-4_COPY_496_599 (1-104) x E10490 (1-1464)
QY      1 Prothrlvleuphiegliuprthrglucysglaenglytrvalgluaaglyglu 20
DB      994 CCCCTCAAGCTCTGGACCCCCCAGAGTGGGAAAGGCTTGTGGAGGCGAGGAG 1053
QY      21 CysAePcysglaPhehisevalglucystyr-----glyleucyselyslsys 37
DB      1054 TGGCAGCTCGGCTCGGTGCAGAGTGCAGCCCGCAGAGTGCAGTCTGTCGCAAGAAATGC 1113
QY      38 SerleuSerAenglyAlahieCysSerAapglProCysCysAaAanThSerCysleu 57
DB      1114 ACCCTGACTCAGCAGCCATGTGCAGCGCGGCTCTGCTGCGCCG-----TGCAAG 1167
QY      58 PheginProAagglYtrYglucysAargAapAlaValaenglyCysAapllethrglu 77
DB      1168 TACGAACCAcGGGGTGTCTCTGCGGAGAGCGCGTGAACGAGTGCAGATCGCGGAGACC 1227
QY      78 CysThrGlyAaPserGlyGlnCysProProAenLeuHiseLysGlnAapglYtrAlaCys 97
DB      1228 TGCACCGGGAGCTTACGACAGTGCAGCGCGCTTAACCTGCACAACTGACGATTACTACTGT 1287
QY      98 AenglnAenglnGlyAargCys 104
DB      1288 GACCATGACAGGCGCGCTGC 1308
RESULT 9
LOCUS      I25845      1464 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 5 from patent US 5552526.
ACCESSION      I25845
VERSION      I25845.1 GI:1605715
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 1464)
AUTHORS      Nakamura, Y. and Eml, M.
TITLE      MDC proteins and DNAs encoding the same
JOURNAL      Patent: US 5552526-A 5 03-SEP-1996;
FEATURES
  source
    1. 1464
    /organism='unknown'
BASE COUNT      294 a      445 c      473 g      252 t
ORIGIN
Alignment Scores:
Pred. No.:      7.01e-33      Length:      1464
Score:          404.50      Matches:      70
Percent Similarity: 73.83%      Conservative: 9
Best Local Similarity: 65.42%      Mismatches: 23
Query Match:    64.21%      Indels:      5

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DB:             Gaps:      2
US-09-634-252A-4_COPY_496_599 (1-104) x I25845 (1-1464)
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QY      21 CysAePcysglaPhehisevalglucystyr-----glyleucyselyslsys 37
DB      1054 TGGCAGCTCGGCTCGGTGCAGAGTGCAGCCCGCAGAGTGCAGTCTGTCGCAAGAAATGC 1113
QY      38 SerleuSerAenglyAlahieCysSerAapglProCysCysAaAanThSerCysleu 57
DB      1114 ACCCTGACTCAGCAGCCATGTGCAGCGCGGCTCTGCTGCGCCG-----TGCAAG 1167
QY      58 PheginProAagglYtrYglucysAargAapAlaValaenglyCysAapllethrglu 77
DB      1168 TACGAACCAcGGGGTGTCTCTGCGGAGAGCGCGTGAACGAGTGCAGATCGCGGAGACC 1227
QY      78 CysThrGlyAaPserGlyGlnCysProProAenLeuHiseLysGlnAapglYtrAlaCys 97
DB      1228 TGCACCGGGAGCTTACGACAGTGCAGCGCGCTTAACCTGCACAACTGACGATTACTACTGT 1287
QY      98 AenglnAenglnGlyAargCys 104
DB      1288 GACCATGACAGGCGCGCTGC 1308
RESULT 10
LOCUS      I43482      1464 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 5 from patent US 5631351.
ACCESSION      I43482
VERSION      I43482.1 GI:2468726
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 1464)
AUTHORS      Nakamura, Y. and Eml, M.
TITLE      Antibodies to MDC proteins
JOURNAL      Patent: US 5631351-A 5 20-MAY-1997;
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    /organism='unknown'
BASE COUNT      294 a      445 c      473 g      252 t
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Pred. No.:      7.01e-33      Length:      1464
Score:          404.50      Matches:      70
Percent Similarity: 73.83%      Conservative: 9
Best Local Similarity: 65.42%      Mismatches: 23
Query Match:    64.21%      Indels:      5
DB:             Gaps:      2
US-09-634-252A-4_COPY_496_599 (1-104) x I43482 (1-1464)
QY      1 Prothrlvleuphiegliuprthrglucysglaenglytrvalgluaaglyglu 20
DB      994 CCCCTCAAGCTCTGGACCCCCCAGAGTGGGAAAGGCTTGTGGAGGCGAGGAG 1053
QY      21 CysAePcysglaPhehisevalglucystyr-----glyleucyselyslsys 37
DB      1054 TGGCAGCTCGGCTCGGTGCAGAGTGCAGCCCGCAGAGTGCAGTCTGTCGCAAGAAATGC 1113
QY      38 SerleuSerAenglyAlahieCysSerAapglProCysCysAaAanThSerCysleu 57
DB      1114 ACCCTGACTCAGCAGCCATGTGCAGCGCGGCTCTGCTGCGCCG-----TGCAAG 1167
QY      58 PheginProAagglYtrYglucysAargAapAlaValaenglyCysAapllethrglu 77
DB      1168 TACGAACCAcGGGGTGTCTCTGCGGAGAGCGCGTGAACGAGTGCAGATCGCGGAGACC 1227

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Oy      78  CyThrGlyAspSerGlyGlnCysProPheLeuHisLysGlnAspGlyTyrAlaCys  97
          |||||
Db      1228 TGCAACGGGGAGCTAGCCAGTGCCTAAGTGCACAGCTGACAGGTTACTACTGT 1287
          |||||
Oy      98  AsnGlnAsnGlnGlyArgCys 104
          |||||
Db      1288 GACCATGAGCAGGGCCGCTGC 1308
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Search completed: October 21, 2003, 12:01:55
Job time : 3441.65 sec8

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:11:41 ; Search time 270.138 Seconds
(without alignments)
1039.251 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599
Perfect score: 630
Sequence: 1 PTKLEPTECGNGYVAGEE.....CPENLHKODGACNONQGRG 104

Scoring table: BLOSUM62
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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	630	100.0	2268	21	AA245826	DNA encoding a dis
2	630	100.0	2268	21	AA511991	Human cDNA encodin
3	630	100.0	2268	24	AB078447	Nucleotide sequenc
4	630	100.0	2499	20	AA210207	CDNA encoding the
5	630	100.0	3054	20	AA210207	Human NDC3 cDNA.
6	630	100.0	3054	25	ABX76201	Lung cancer-associ
7	630	100.0	3054	25	ABX76202	Lung cancer-associ
8	630	100.0	4043	25	AA172025	ADAM 23 cDNA. Hom
9	566	93.0	1668	22	AA212136	ADAM-23dis-Fc fusi
10	567	90.0	2088	21	AA245827	Degenerate DNA enc
11	567	90.0	2088	22	AA511992	Human degenerate D
12	567	90.0	2088	24	AB078448	Degenerate nucleot
13	404.5	64.2	1464	16	AA076119	Human fetal cerebe
14	404.5	64.2	2913	16	AA076120	Human fetal cerebe
15	404.5	64.2	2913	16	AA076120	Human fetal cerebe
16	404.5	64.2	3183	16	AA076122	Human fetal brain
17	363.5	57.7	2604	20	AA210208	CDNA encoding the
18	363.5	57.7	2697	20	AA210208	Human MDC2-beta cD
19	363.5	57.7	2805	20	AA210208	Human MDC2-beta cD
20	338.5	53.7	1674	22	AA21438	ADAM-22dis-Fc fusi
21	292	46.3	2642	24	AB086500	Human novel protei
22	292	46.3	2649	24	AA597181	Human novel protei
23	292	46.3	2705	24	AB084499	Human metallopept
24	292	46.3	2762	24	AB084498	Human novel protei
25	292	46.3	3431	22	AA085513	First splice varia
26	292	46.3	3431	24	AB072136	Nucleotide sequenc
27	292	46.3	3466	24	AB066136	CDNA encoding huma
28	292	46.3	3468	22	AA085514	Second splice vari
29	292	46.3	3468	24	AB072137	Nucleotide sequenc
30	292	46.3	3509	23	AB072025	Gene 216 alternati
31	292	46.3	3509	25	ABX74890	Human gene 216 cDN
32	292	46.3	3582	22	AA046157	Human DNA encoding
33	292	46.3	3582	25	AA046157	Human PRO1891 cDNA
34	292	46.3	3582	25	ABX98385	Human cDNA encodin
35	292	46.3	3582	25	ABX98887	Human cDNA encodin
36	292	46.3	3582	25	AA059312	Human secreted/tra
37	292	46.3	3582	25	ABX97976	Human PRO polynuc
38	292	46.3	3582	25	ABX78760	Human PRO polynuc
39	292	46.3	3582	25	ABX75773	Human cDNA encodin
40	292	46.3	3582	25	ABX76878	Human PRO polynuc
41	292	46.3	3582	25	ABX16818	Human cDNA encodin
42	292	46.3	3626	23	AB072023	Gene 216 encoding
43	292	46.3	3626	25	ABX74888	CDNA encoding huma
44	279	44.3	1638	22	AA021434	ADAM-15dis-Fc fusi
45	278	44.1	2653	17	AA034616	CRII-7 nerve prote

ALIGNMENTS

RESULT 1
AA245826
ID AA245826 standard; DNA: 2268 BP.
XX
AC AA245826;
XX
DT 25-APR-2000 (first entry)
XX
XX DNA encoding a disintegrin homologue designated zdint1.
XX
XX Human: disintegrin homologue; zdint1; cardiac myocyte; adipocyte;
KW gene therapy; cell-cell interaction; chondro sarcoma; atherosclerosis;
KW Alzheimer's disease; resperosis; ischemic reperfusion; obesity;
KW intestinal hyperplasia; tumour; platelet aggregation; apoptosis;
KW neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
KW connective tissue disorder; chondrogenesis; tumour proliferation;
KW inflammation; ss.

XX OS Homo sapiens. Location/Qualifiers
 XX FH Key 3.2093
 XX FT CDS /tag= a
 XX FT /product= "zdint1"
 XX PN WO200002912-A2.
 XX PD 20-JAN-2000.
 XX PF 09-JUL-1999; 99WO-US15638.
 XX PR 10-JUL-1998; 98US-0113883.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Sheppard PO, Baindur N, Deisher TA, Bishop PD,
 XX DR WPI; 2000-160898/14.
 XX P-PSDB; AAY54457.
 XX PT Polypeptide useful in modulating cell-cell interaction in tissues of
 XX heart, brain, spinal cord and treating chondro sarcoma,
 XX PT atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -
 XX PS Example 1; Page 123-127; 132pp; English.

The present sequence encodes a human disintegrin homologue, designated
 zdint1. The zdint1 polypeptide is a cardiac myocyte proliferation and
 differentiation stimulator, as well as an adipocyte proliferation and
 differentiation inhibitor. Polynucleotides encoding zdint1 are used in
 gene therapy. The zdint1 polypeptide is useful in modulating cell-cell
 interactions of cells derived from tissues of heart, brain, spinal cord
 and skeletal muscle. It is useful in treating and diagnosing chondro
 sarcoma, atherosclerosis, Alzheimer's disease, restenosis, ischemic
 reperfusion, obesity, intimal hyperplasia and tumors of heart, brain,
 and spinal cord. The zdint1 polypeptide is also useful in identifying
 its new family members, antagonists, agonists and antibodies.
 CC Antagonists, antibodies and fusion proteins of zdint1 are useful in
 CC inhibiting platelet aggregation, apoptosis, neurogenesis and myogenesis.
 CC Agonists and antagonists are useful in studying cell-cell interactions.
 CC arthritis, myogenesis, neurogenesis, connective tissue disorders,
 CC chondrogenesis, tumor proliferation and suppression, extracellular
 CC matrix proteins, repair and remodelling of ischemic reperfusion,
 CC inflammation, and apoptosis.

SO Sequence 2268 BP; 654 A; 457 C; 558 G; 598 T; 1 other;

Alignment Scores:
 Pred. No.: 3.49e-55 Length: 2268
 Score: 630.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AA245826 (1-2268)

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 Db 1119 CCMAAAGAGCTATTGAGCCCGAGAAATGCTGAAGAGCTGGAGAGAG 1178
 QY 21 CysAspCysglYPhEhIValGluCysTYrGlyLeuCysCysValYsCysSerLeuSer 40
 Db 1179 TGTGATTGTGTTTCACTGGAATGCTATGATGCTGTAAGAAATGTTCCCTCTCC 1238
 QY 41 AAsnglyAlAsCysSerAspGlyProCysCysAAsnAsnThSerCysLeuPhGlnPro 60
 Db 1239 AACGGGGCTCACTGAGCGAGCGAGCGCCCTGCTTAACAATACCTCATGCTTTTACGCA 1298
 QY 61 ArgGlyTYrGluCysArgAspAlaValAsngluCysAspIleThrGluTYrCysThrgly 80

Db 1299 CGAGGTAATGATCCCGGAGTCTGTGAACAGTGTGATATTAAGTAATTTGTAAGTGA 1358
 QY 81 AspSerGlyGlnCysProProAsnLeuHIsyGlnAspGlyTYrAlaCysAsnGlnAsn 100
 Db 1359 GACTCTGGTCAGTGCACCAAAATCTTCAATGAAGACAGATATGCAATCAAAAT 1418
 QY 101 GlnGlyArgCys 104
 Db 1419 CAGGGCCGCTGC 1430

RESULT 2
 AAS11991
 ID AAS11991 standard; CDNA; 2268 BP.

AC AAS11991;

DT 04-DEC-2001 (first entry)

DE Human CDNA encoding partial disintegrin protease zdint1.

Human; disintegrin; zdint1; ss; antiangiogenic; vascular; thrombolytic.
 cell matrix; cell-cell interactions; apoptosis; neurogenesis;
 connective tissue disorders; chondrogenesis; arthritis;
 tumor proliferation; ischemia reperfusion; inflammation;
 chromosome 2q33.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT CDS 3.2093
 FT /tag= a
 FT /product= "zdint1"
 FT /partial
 FT /note= "No start codon"
 FT sig_peptide 3.491
 FT /tag= b
 FT /note= "Encodes propeptide sequence"
 FT mat_peptide 492..2090
 FT /tag= c
 FT /label= Mature_zdint1

XX US6265199-B1.
 XX 24-JUL-2001.
 XX 09-JUL-1999; 99US-0351414.
 XX 10-JUL-1998; 98US-0092371.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Baindur N, Deisher TA, Bishop PD, Taft DW,
 XX WPI; 2001-450736/48.
 XX P-PSDB; AAU07190.

Disintegrins protease zdint1, useful for producing agents for the
 development of antithrombotic and anti-migration of tumour cells and
 have antiangiogenic activity -
 Example 1; Column 47-53; 50pp; English.

The invention relates to an isolated novel disintegrin protease family
 member, zdint1. Disintegrins bind cell surface molecules, including
 integrins, on the surface of various cells such as platelets,
 fibroblasts, tumor, endothelial, muscle, neuronal, bone and sperm cells.
 CC Disintegrins are unique and potentially useful tools for investigating
 CC cell matrix and cell-cell interactions, apoptosis, neurogenesis,
 CC connective tissue disorders, chondrogenesis, arthritis, tumor
 CC proliferation, ischemia reperfusion and inflammation. Additionally, they
 CC are useful in the development of antithrombotic and anti-migration of
 CC tumour cells and have antiangiogenic activity. The present sequence

CC encodes human disintegrin, zdn1c1, the gene for which is located on
CC chromosome 2q33.

Sequence 2268 BP; 654 A; 457 C; 558 G; 598 T; 1 other;

Alignment Scores:

Pred. No.:	3,496-55	Length:	2268
Score:	630.00	Matches:	104
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-634-252a-4_COPY_496_599 (1-104) x AAS11991 (1-2268)

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DB 1119 CCAACAAAGCTATTGAGCCCGAATGTGAAATGATACGTGAAAGCTGGGAGAG 1178
QY 21 CysAspCysGlyPheHisValGluCySTYrGlyLeuCySCySlyblybCySerLeuSer 40
DB 1179 TGTGATTGTGGTTTTCATGTGGAATGCTATGATATGCTGTAAATAATGTTCCCTCTCC 1238
QY 41 AsnGlyAlaHisCysSerAspGlyProCySCysAsnAsnThrSerCysLeuPheGlnPro 60
DB 1239 AACGGGCTCAGTCAGCCAGCGGCGCTGTAAACATACCTCTCTTTTTCAGCCA 1298
QY 61 ArgGlyTYrGluCysAspAspAlaValAsnGluCysAspIleThrGluTYrCysThrGly 80
DB 1299 CGAGGGTATGAATGCCGGAGATGCTGTAAACAGTGTATATTAAGTAATGTACTGGA 1358
QY 81 AspSerGlyGlnCysProProAsnLeuHisGlyGlnAspGlyTYrAlaCysAsnGlnAsn 100
DB 1359 GACTCTGTGTCAGTCCCAACCAATCTTCATAGCAACAGGATATGATGCAATCAAAAT 1418
QY 101 GlnGlyArgCys 104
DB 1419 CAGGGCGCTGC 1430
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RESULT 3

ABQ78447 ID ABQ78447 standard; cDNA; 2268 BP.

AC ABQ78447;

DT 05-NOV-2002 (first entry)

XX Nucleotide sequence of human zdn1c1.

XX Human; zdn1c1; disintegrin protease; platelet accumulation;
XX chromosome 2q33; platelet aggregation; proteolysis; apoptosis;
XX neurogenesis; myogenesis; connective tissue disorder; arthritis;
XX chondrogenesis; cell adhesion; cell fusion; neuron; myocyte; heart;
XX brain; spinal cord; skeletal muscle tissue; Alzheimer's disease;
XX tumour formation; multiple sclerosis; congestive heart failure;
XX ischaemic reperfusion; intimal hyperplasia; restenosis; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 3..2093

XX FT /*cag= a

XX FT /product= "zdn1c1"

XX PN US2002072102-A1.

XX PD 13-JUN-2002.

XX PF 16-MAR-2001; 2001US-0809790.

XX PR 10-JUL-1998; 98US-092371P.

XX PR 09-JUL-1999; 99US-0351414.

XX XX

PA (SHEP/) SHEPPARD P O.
PA (BAIN/) BAINDUR N.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.

PI Sheppard PO, Baidur N, Deisher TA, Bishop PD;

XX WPI; 2002-598452/64.

XX P-PSDB; ABB78130.

PT New disintegrin homolog polypeptide and polynucleotide, useful for
PT modulating cell-cell interactions and diagnosis, treatment of
PT Alzheimer's disease, tumour formation, multiple sclerosis and congestive
PT heart failure

PS Claim 14; Page 26-29; 53pp; English.

CC The present sequence encodes a human polypeptide designated zdn1c1.
CC zdn1c1 is a member of the disintegrin protease family. zdn1c1 inhibits
CC platelet accumulation. The zdn1c1 gene is present on chromosome 2q33.
CC zdn1c1 polypeptides and polynucleotides are useful in treatment of
CC disorders associated with infarct in brain or heart tissue and/or
CC platelet aggregation, to modulate proteolysis, apoptosis, neurogenesis,
CC myogenesis, connective tissue disorders, arthritis, chondrogenesis,
CC cell adhesion, cell fusion, and signalling or to treat or prevent
CC development of pathological conditions in such diverse tissue as heart,
CC brain, spinal cord and skeletal muscle. The molecules modulate
CC inhibition and proliferation of neurons and myocytes in heart, brain,
CC spinal cord and skeletal muscle tissue. Disorders which may be amenable
CC to diagnosis, treatment or prevention with zdn1c1 polypeptides include,
CC Alzheimer's disease, tumour formation, multiple sclerosis, congestive
CC heart failure, ischaemic reperfusion or infarct and degenerative
CC diseases. The zdn1c1 molecules particularly useful in the treatment of
CC intimal hyperplasia or restenosis due to acute vascular injury.

XX Sequence 2268 BP; 654 A; 457 C; 558 G; 598 T; 1 other;

Alignment Scores:

Pred. No.:	3,496-55	Length:	2268
Score:	630.00	Matches:	104
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-634-252a-4_COPY_496_599 (1-104) x ABQ78447 (1-2268)

```
QY 1 ProThrIysLeuPheGluProThrGluCySGIYASnGIYrYValGluAgiYgluGlu 20
DB 1119 CCAACAAAGCTATTGAGCCCGAATGTGAAATGATACGTGAAAGCTGGGAGAG 1178
QY 21 CysAspCysGlyPheHisValGluCySTYrGlyLeuCySCySlyblybCySerLeuSer 40
DB 1179 TGTGATTGTGGTTTTCATGTGGAATGCTATGATATGCTGTAAATAATGTTCCCTCTCC 1238
QY 41 AsnGlyAlaHisCysSerAspGlyProCySCysAsnAsnThrSerCysLeuPheGlnPro 60
DB 1239 AACGGGCTCAGTCAGCCAGCGGCGCTGTAAACATACCTCTCTTTTTCAGCCA 1298
QY 61 ArgGlyTYrGluCysAspAspAlaValAsnGluCysAspIleThrGluTYrCysThrGly 80
DB 1299 CGAGGGTATGAATGCCGGAGATGCTGTAAACAGTGTATATTAAGTAATGTACTGGA 1358
QY 81 AspSerGlyGlnCysProProAsnLeuHisGlyGlnAspGlyTYrAlaCysAsnGlnAsn 100
DB 1359 GACTCTGTGTCAGTCCCAACCAATCTTCATAGCAACAGGATATGATGCAATCAAAAT 1418
QY 101 GlnGlyArgCys 104
DB 1419 CAGGGCGCTGC 1430
```

RESULT 4

AA210207

AA210207 standard; DNA; 2499 BP.

AA210207;

29-OCT-1999 (first entry)

CDNA encoding the human SVP3-17 protein.

SVP3-17; metalloproteinase-disintegrin; human chromosome 2; human chromosome 7; malignant hyperthermia susceptibility; Zellweger Refsum disease; neonatal adrenoleukodystrophy; infantile Refsum disease; progressive familial intrahepatic cholestasis; mucopolysaccharidosis VII; split hand/foot malformation; arylthymogenic right ventricular dysplasia-4; Coppock-like cataract; insulin dependent diabetes mellitus-12; lamellar type ichthyosis; transient neonatal myasthenia gravis; congenital aculeiform cataract; juvenile amyotrophic lateral sclerosis; familial paroxysmal choreoathetosis; Finnish lethal neonatal metabolic syndrome; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 1..2499

/*tag= a

MO3941388-A2.

19-AUG-1999.

11-FEB-1999; 99WO-US03016.

11-FEB-1998; 98US-0074310.

(IMMV) IMMUNEX CORP.

Corrected DP;

WPI; 1999-527371/44.

P-PSDB; AAY30207.

DNA encoding the SVP3-13 and SVP3-17 proteins for detecting disease corresponding to chromosome 7, e.g. Zellweger syndrome

Claim 1; Page 7-8; 82pp; English.

The present sequence encodes a protein designated SVP3-17, which is a member of the metalloproteinase-disintegrin family. The specification also describes SVP3-13 proteins. Both sequences can be used to identify human chromosome 2 or 7, and to map genes on these two chromosomes, and also to identify genes associated with certain diseases, syndromes, or other human conditions associated with human chromosome 2 or 7. The disease that correspond to chromosome 7 include malignant hyperthermia susceptibility; Zellweger syndrome; neonatal adrenoleukodystrophy; infantile Refsum disease; progressive familial intrahepatic cholestasis; mucopolysaccharidosis VII, and split hand/foot malformation. Diseases associated with chromosome 2 include arylthymogenic right ventricular dysplasia-4, insulin dependent diabetes mellitus-12, transient neonatal myasthenia gravis, juvenile amyotrophic lateral sclerosis, congenital aculeiform cataract, Coppock-like cataract, lamellar type ichthyosis, familial paroxysmal choreoathetosis, and Finnish lethal neonatal metabolic syndrome.

Sequence 2499 BP; 677 A; 593 C; 645 G; 584 T; 0 other;

Alignment Scores:

Pred. No.: 3,95e-55 Length: 2499

Score: 630.00 Matches: 104

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 20 Gaps: 0

US-09-634-252A-4_COPY_496_599 (1-104) x AA210207 (1-2499)

OY 1 ProthrlvlsleuphagluProthrGluCysGlyAenglyTyValAGluAGluGlu 20

DB 1486 CCAACAAAGCTATTGAGCCCAAGGAAATGTGGAATGATACGTGGAAGCTGGGAGAG 1545

OY 21 CysAspCysGlyPheHisValGluCysTyrGlyLeuCysLysLysCysSerLeuSer 40

DB 1546 TGTGATGTGCTTTTCATGATGGAATGCTATGATGATGCTGTAAGAAATGTTCCCTCC 1605

OY 41 AenglyAlaHisCysSerAspGlyProCysCysAsnAntTrsSerCysLeuPheGlnPro 60

DB 1666 AACGGGCTCATCGAGGAGGAGGCGCTCGTAACAATACCTCATGCTTTTCAGCCA 1665

OY 61 ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGly 80

DB 1666 CGAGGATGAAATGCCGGATGCTGTGACAGTGTGATATTACTGAATATTGACTGA 1725

OY 81 AspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsn 100

DB 1726 GACTCTGCTCAGTGCCCAACCAATCTTCATAGCAAGACGATGATGCAATCAAAAT 1785

OY 101 GlnGlyArgCys 104

DB 1786 CAGGCCCGCTGC 1797

RESULT 5

AA278438

ID AA278438 standard; CDNA to mRNA; 3054 BP.

XX AA278438;

AC 26-AUG-1999 (first entry)

XX 26-AUG-1999 (first entry)

DT 26-AUG-1999 (first entry)

XX 26-AUG-1999 (first entry)

DE Human MDC3 CDNA.

XX Metalloproteinase-like-disintegrin-like cysteine rich protein; human;

KW MDC2-alpha; MDC2-beta; MDC3; medical; treatment; diagnosis; ds.

OS Homo sapiens.

Key Location/Qualifiers

CDS 224..2722

FT /*tag= a

FT /*product= "MDC3"

XX JP1155574-A.

XX 15-JUN-1999.

XX 01-DEC-1997; 97JP-0330020.

XX 01-DEC-1997; 97JP-0330020.

XX (EISA) EISAI CO LTD.

PA WPI; 1999-398071/34.

DR P-PSDB; AAY25120.

PT New protein belonging to MDC gene family - useful in medical

PT treatment and diagnosis

PS Claim 17; Page 13-16; 17pp; Japanese.

XX This invention describes novel human MDC2-alpha, MDC2-beta and MDC3

CC proteins and their encoding nucleic acids. The products of the invention

CC are useful in medical treatment and diagnosis.

SO Sequence 3054 BP; 815 A; 754 C; 803 G; 682 T; 0 other;

Alignment Scores:

Pred. No.: 5,08e-55 Length: 3054

Score: 630.00 Matches: 104

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 20
Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AAX78438 (1-3054)

Qy 1 ProThrlsLeuphegluProThrgluCysglYasnclYTyrraJgluaJgluGlu 20
Db 1709 CCAACAAAGCTATTGGAGCCACCGAATGCGAATGATACGTGGAAGCTGGGAGAG 1768
Qy 21 CysaspCysglYpnehlsvaJgluCystrYglYleuCYslyslYsCYsSerleuSer 40
Db 1769 TGTATTGTGTTTTTCATGATGGAATGCTATGCTTAAAGAAATGTTCCCTCC 1828
Qy 41 AsnGlylaHlsCYsSerAspGlyProCYsCYsAsnaHnRserCYsleuPhglPro 60
Db 1829 AACGGGCTCACTGACGAGCGAGGCGCTGCTGTAACATACCTCTGCTTTTCAGCCA 1888
Qy 61 ArgGlyTyrgluCYsArgAspAlaValAsnGluCYsAspIlethrgluTyrcYstrGly 80
Db 1889 CGAGGATGATGAATCGCGGATGCTGTGAACGAGTGTATTTACTGATATTGTACTGA 1948
Qy 81 AspserGlyGlnCYsProProAsnleuHlsYsglnAspGlyTyrraJCYsAsnGlnAsn 100
Db 1949 GACTCTGTGTCAGTCCACCAAACTTTCATTAAGCAAGCATATGCAATCAAAAT 2008
Qy 101 GlnGlyArGys 104
Db 2009 CAGGCGCGCTGC 2020

RESULT 6

ABX76201
ID ABX76201 standard; DNA; 3054 BP.

AC ABX76201;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polynucleotide #72.

KM Lung cancer-associated polynucleotide; gene: ds; cytotatic; emphysema;
antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

OS Unidentified.

PN MO200286443-A2.

PD 31-OCT-2002.

PF 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.

PR 09-NOV-2001; 2001US-339245P.

PR 13-NOV-2001; 2001US-350666P.

PR 29-NOV-2001; 2001US-374370P.

PR 12-APR-2002; 2002US-372246P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PI Aziz N, Murray R;

DR WPI; 2003-093161/08.

DR P-PSDB; ABUS6479.

XX

XX Claim 22; Page 243; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
CC polynucleotides of the invention.

XX S0 Sequence 3054 BP; 815 A; 754 C; 803 G; 682 T; 0 other;

Alignment Scores:

Pred. No.: 5,08e-55 Length: 3054
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x ABX76201 (1-3054)

Qy 1 ProThrlsLeuphegluProThrgluCysglYasnclYTyrraJgluaJgluGlu 20
Db 1709 CCAACAAAGCTATTGGAGCCACCGAATGCGAATGATACGTGGAAGCTGGGAGAG 1768
Qy 21 CysaspCysglYpnehlsvaJgluCystrYglYleuCYslyslYsCYsSerleuSer 40
Db 1769 TGTATTGTGTTTTTCATGATGGAATGCTATGCTTAAAGAAATGTTCCCTCC 1828
Qy 41 AsnGlylaHlsCYsSerAspGlyProCYsCYsAsnaHnRserCYsleuPhglPro 60
Db 1829 AACGGGCTCACTGACGAGCGAGGCGCTGCTGTAACATACCTATGCTTTTCAGCCA 1888
Qy 61 ArgGlyTyrgluCYsArgAspAlaValAsnGluCYsAspIlethrgluTyrcYstrGly 80
Db 1889 CGAGGATGATGAATCGCGGATGCTGTGAACGAGTGTATTTACTGATATTGTACTGA 1948
Qy 81 AspserGlyGlnCYsProProAsnleuHlsYsglnAspGlyTyrraJCYsAsnGlnAsn 100
Db 1949 GACTCTGTGTCAGTCCACCAAACTTTCATTAAGCAAGCATATGCAATCAAAAT 2008
Qy 101 GlnGlyArGys 104
Db 2009 CAGGCGCGCTGC 2020

RESULT 7

ABX76292
ID ABX76292 standard; DNA; 3054 BP.

AC ABX76292;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polynucleotide #156.

KM Lung cancer-associated polynucleotide; gene: ds; cytotatic; emphysema;
antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

Unidentified.

MO200286443-A2.

31-OCT-2002.

18-APR-2002; 2002WO-US12476.

18-APR-2001; 2001US-284770P.

10-MAY-2001; 2001US-290492P.

09-NOV-2001; 2001US-339245P.

13-NOV-2001; 2001US-350666P.

29-NOV-2001; 2001US-334370P.

12-APR-2002; 2002US-372246P.

(EOSB-) EOS BIOTECHNOLOGY INC.

Aziz N, Murray R.

WPI; 2003-093161/08.

P-PSDB; ABUS6563.

Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

Claim 22; Page 307-308; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention.

Sequence 3054 BP; 815 A; 754 C; 803 G; 682 T; 0 other;

Alignment Scores:

Pred. No.: 5,08e-55 Length: 3054

Score: 630.00 Matches: 104

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x ABX76292 (1-3054)

ProtrNlysluPhuGluProThrgluCysGlyAenGlyTyValGluAlaGluGluGlu 20

1709 CCAACAAAGCTATTGAGCCCGACGAAATGTGAATGATGATGAGAACTGGAGAGAG 1768

21 CysAspCysGlyPheHisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSer 40

1769 TGTGATTGGTTCATGATGGAATGCTATGATGATGATGATGATGATGATGATGATGAT 1828

41 AenGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGluPro 60

1829 AACGGGCTCACTGACGAGCGGCCCTGCTGTAAACAATACCTGCTTTTCAGCCA 1888

ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlyThrGly 80

1889 CGAGGTATGATGATGCGGAGATGCTGTGAACAGTGTGATATTACTGAATATTGATCGA 1948

81 AspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsn 100

1949 GACTCTGTCAGTGTGCCACCAACATCTTCATAGCAAGACGATATGATGCAATCAAAAT 2008

101 GlnGlyArgCys 104

2009 CAGGCCCGCTGC 2020

RESULT 8

AA172025

AA172025 standard; cDNA, 4043 BP.

AA172025;

04-MAR-2002 (first entry)

ADAM 23 cDNA.

Disintegrin; ADAM 23; metalloproteinase; domain; adhesion; proteolysis; modulator; alpha-v-beta3 integrin; tumour progression; neural tissue; angiogenesis; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 1017..3515

FT /*tag= a

FT /product= "ADAM 23"

WO200174857-A2.

11-OCT-2001.

02-APR-2001; 2001WO-US10729.

03-APR-2000; 2000US-194164P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Lopez-Otin C, Freije JMP, Bianchi AB, Miguel SC, Garcia JML; Trial 1;

WPI; 2002-066298/09.

P-PSDB; AAB47778.

Nucleic acid encoding a new ADAM family member, designated ADAM 23 is useful to find modulators of its interaction with integrin which can be used to prevent angiogenesis or increase neural growth.

Claim 2; Page 36-38; 44pp; English.

This sequence encodes a cellular disintegrin, ADAM 23, which is a protein having a disintegrin and metalloproteinase domain. This protein can perform both adhesion and proteolytic functions. Modulators of the interaction between ADAM and alpha-v-beta3 integrin are used to inhibit tumour progression or induce growth of neural tissue. These compounds modulate angiogenesis and induction of matrix metalloproteinases facilitating migration of tumour cells and growth of neural tissue.

Sequence 4043 BP; 1110 A; 946 C; 1002 G; 985 T; 0 other;

Alignment Scores:

Pred. No.: 7.21e-55 Length: 4043

Score: 630.00 Matches: 104

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AA172025 (1-4043)

QY 1 ProthrtlystleupheglnpProthrglucy6glvenglytyrvalgluaaglglu 20
 DB 2502 CCACCAAGCTATTGAGCCACCGAATGTGGAAATGATACGTAAGAGCTGGGAGAG 2561

QY 21 CysAspCy6glvPhenHsValGlcY6sTyrglyLeuCy6sLysLysCy6sSerLeuSer 40
 DB 2562 TGTGATTGTGTTTTCATGTGGAATGCTATGGAATTAAGCTTAAGAAATGTTCCCTCTCC 2621

QY 41 AsnGlyAlahisCy6sSerAspGlyProCy6sCysAsnAnthrSe:CYeLeupheglnPro 60
 DB 2622 AACGGGCTCACTCAGAGAGAGGGCCCTGCTGTAACATACCTCATGCTTTTCACGCA 2681

QY 61 ArgGlytyrGluCy6sArgAspAlaValAsnGluCy6sAspIlethrglytyrCy6sThrgly 80
 DB 2682 CGAGGGTATGATGTCGCGGATGCTGTAAACAGAGTGTATATACGTAATATTGACTGGA 2741

QY 81 AspserGlyGlnCy6sProAsnLeuHlsyGlnAspGlytyrAlaCy6sAsnGlnAsn 100
 DB 2742 GACTCTGCTAGTCCCAACATCTTCATTAAGCAAGCGATATGCAATCAAAAT 2801

QY 101 GlnGlyArgCys 104
 DB 2802 CAGGGCCGCTGC 2813

RESULT 9
 AAD21439 standard; DNA, 1668 BP.

AC AAD21439:
 XX 28-JAN-2002 (first entry)
 XX ADAM-23dis-Fc fusion construct DNA.

DE ADAM-23dis-Fc fusion construct DNA.

XX Human; ADAM disintegrin domain; integrin; endothelial cell migration;
 KM angiogenesis; ocular disorder; inflammatory disease; bone resorption;
 KM osteoporosis; restenosis; thrombosis; tissue repair; wound healing;
 KM retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
 KM retrolental fibroplasia; inflammatory bowel disease; rubecosis; uveitis;
 KM arthritis; rheumatism; myocardial infarction; coronary artery disease;
 KM tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;
 KM preclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;
 KM Igk; Fc region; antiinflammatory; osteopathic; vasotropic; thrombolytic;
 KM ds.

XX OS Chimeric - Homo sapiens.
 OS Chimeric - Unidentified.

XX FH Key Location/Qualifiers
 FT CDS 25..1647
 FT FT /*tag= a
 FT FT /product= "ADAM-23dis-Fc fusion construct"
 FT FT 25..84
 FT FT /*tag= b
 FT FT /note= "Igk leader sequence"
 FT FT 85..1644
 FT FT /*tag= c
 FT FT /product= "Mature ADAM-23dis-Fc fusion construct"
 FT FT 93..954
 FT FT /*tag= d
 FT FT /note= "Human ADAM disintegrin"
 FT FT 963..1644
 FT FT /*tag= e
 FT FT /note= "Fc region"
 XX PN WO200162905-A2.
 XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US05701.
 PF 25-FEB-2000; 2000US-184865P.
 PR (IMMUNEX CORP.
 PA Fanslow WC, Cerretti DP, Poindexter KM, Black RA;
 PI WPI: 2001-625725/72.
 DR P-PSDB: AAE13059.
 XX Antagonizing the binding of an integrin to its ligand useful for the
 PT treatment of angiogenesis comprises administration of an
 PT ADAM-disintegrin domain polypeptide
 XX Claim 14; Page 58-60; 66pp; English.

PS The invention relates to the method and use of ADAM disintegrin domain
 CC polypeptides for inhibiting the biological activity of integrins,
 CC endothelial cell migration and angiogenesis. ADAM disintegrin domain
 CC polypeptides are used for treatment of ocular disorders, malignant and
 CC metastatic conditions, inflammatory diseases, osteoporosis and other
 CC conditions mediated by accelerated bone resorption, restenosis,
 CC inappropriate platelet activation, recruitment or aggregation, thrombosis
 CC or a condition requiring aggregation, thrombosis or a condition requiring
 CC tissue repair or wound healing, angiogenesis, ocular neovascularisation
 CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,
 CC neovascular glaucoma, retinoblastoma, retrolental fibroplasia, rubecosis,
 CC uveitis, macular degeneration and corneal graft neovascularisation.
 CC inflammatory diseases, ocular tumours, diseases associated with choroidal
 CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel
 CC disease, psoriasis, coronary artery disease or injury, myocardial
 CC infarction or injury following myocardial infarction, stroke, unstable
 CC angina, atherosclerosis, arteriosclerosis, preclampsia, embolism,
 CC platelet-associated ischaemic disorders including lung ischaemia,
 CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
 CC coronary intervention including angioplasty, atherectomy, stent placement
 CC and bypass surgery, thrombotic disorders including coronary artery
 CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis and
 CC coagulopathies associated with exposure to a foreign or injured tissue
 CC surface and reocclusion following thrombosis, deep venous thrombosis,
 CC pulmonary embolism, transient ischaemic attacks and another conditions
 CC where vascular occlusion is a common underlying feature. In individuals
 CC at high risk for thrombus formation of reformation, advanced coronary
 CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis
 CC of blood vessels or stroke benign tumours and preneoplastic conditions,
 CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular
 CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host
 CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and
 CC wound granulation. The method are used in combination with angioplasty
 CC procedures, such as balloon angioplasty, laser angioplasty, coronary
 CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of
 CC vascular grafts, surgery having a high risk of thrombus formation (i.e.
 CC coronary bypass surgery, insertion of a prosthetic valve or vessel and
 CC the like), atherectomy, stent placement, placement of a chronic
 CC cardiovascular device such as an in-dwelling catheter or prosthetic valve
 CC or vessel, organ transplantation or bypass surgery. The present sequence
 CC is a DNA encoding ADAM disintegrin domain polypeptide fusion construct.
 CC The fusion construct comprises of immunoglobulin K (Igk) leader, human
 CC ADAM disintegrin and Fc region.

XX Sequence 1668 BP; 423 A; 444 C; 455 G; 346 T; 0 other;

SO Alignment Scores:
 Pred. No.: 8,15e-51 Length: 1668
 Score: 586.00 Matches: 96
 Percent Similarity: 98.97% Conservative: 0
 Best Local Similarity: 98.97% Mismatches: 1
 Query Match: 93.02% Indels: 0
 DB: 22 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AAD21439 (1-1668)

QY 8 ThrGluCysGlyAsnGlyTyrValGluAlaGluGluCysAspCysGlyPheHisVal 27
 DB 85 ACTACTGTGGAAAGCATACCTCCGAAGCTGGGAGAGACTGATGTTGCTTTTATGTG 144

QY 28 GluCyTYrGlyLeuCyCysAlaGlySerLeuSerAsnGlyAlaHisCysSerAsp 47
 DB 145 GAATGCTATGATATGCTGTAAGAAATGTCCTCTCCCAACGGGGCTCAGCAGCGAC 204

QY 48 GlyProCysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTYrGluCysArgAsp 67
 DB 205 GGGCCCTGCTGAACAATACCTCATGCTTTTTCAGCCACGAGGATATGAAGCCGGGAT 264

QY 68 AlaValAsnGluCysAspIleThrGluTYrCysThrGlyAspSerGlyGlnCysProPro 87
 DB 265 GCTGTGAACGAGTGCATATTTCTGAATTTTACTGAGACTCTGGTCAGTCCACCA 324

QY 88 AsnLeuHisLysGlnAspGlyTYrAlaCysAsnGlnAsnGlnGlyArgCys 104
 DB 325 AATCTTCATTAACCAAGACCGATATGATCATCAAAATCAGGCGGCTGC 375

RESULT 10
 ID AAZ45827 standard; DNA; 2088 BP.

AC AAZ45827;
 AC AAZ45827;
 DT 25-APR-2000 (first entry)

DE Degenerate DNA encoding a disintegrin homologue designated zdint1.
 XX
 XX Human; disintegrin homologue; zdint1; cardiac myocyte; adipocyte;
 KW gene therapy; cell-cell interaction; chondro sarcoma; atherosclerosis;
 KW Alzheimer's disease; restenosis; ischemic reperfusion; obesity;
 KW intimal hyperplasia; tumour; platelet aggregation; apoptosis;
 KW neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
 KW connective tissue disorder; chondrogenesis; tumour proliferation;
 KW inflammation; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO200002912-A2.
 PN
 XX
 XX 20-JAN-2000.
 PD
 XX
 XX 09-JUL-1999; 99WO-US15638.
 PF
 XX
 XX 10-JUL-1998; 98US-0113883.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Sheppard PO, Baindur N, Deisher TA, Bishop PD;
 PI
 XX
 XX WPI; 2000-160898/14.
 DR
 XX
 XX Poly peptide useful in modulating cell-cell interaction in tissues of
 PT heart, brain, spinal cord and treating chondro sarcoma,
 PT atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -
 XX
 XX
 PS Disclosure; Page 129-130; 132pp; English.
 CC
 CC The present sequence represents a degenerate sequence which encodes
 CC a human disintegrin homologue, designated zdint1. The zdint1 polypeptide
 CC is a cardiac myocyte proliferation and differentiation stimulator, as
 CC well as an adipocyte proliferation and differentiation inhibitor.
 CC Polynucleotides encoding zdint1 are used in gene therapy. The zdint1
 CC polypeptide is useful in modulating cell-cell interactions of cells
 CC derived from tissues of heart, brain, spinal cord and skeletal muscle.
 CC It is useful in treating and diagnosing chondro sarcoma, atherosclerosis,
 CC Alzheimer's disease, restenosis, ischemic reperfusion, obesity, intimal
 CC hyperplasia and tumors of heart, brain, and spinal cord. The zdint1

CC polypeptide is also useful in identifying its new family members,
 CC antagonists, agonists and antibodies. Antagonists, antibodies and fusion
 CC proteins of zdint1 are useful in inhibiting platelet aggregation,
 CC apoptosis, neurogenesis and myogenesis. Agonists and antagonists are
 CC useful in studying cell-cell interactions, arthritis, myogenesis,
 CC neurogenesis, connective tissue disorders, chondrogenesis, tumour
 CC proliferation and suppression, extracellular matrix proteins, repair
 CC and remodeling of ischemic reperfusion, inflammation, and apoptosis.

XX
 XX
 XX Sequence 2088 BP: 412 A; 178 C; 381 G; 262 T; 855 other;

Alignment Scores:
 Pred. No.: 9, 81e-49 Length: 2088
 Score: 567.00 Matches: 91
 Percent Similarity: 87.50% Conservative: 0
 Best Local Similarity: 87.50% Mismatches: 13
 Query Match: 90.00% Indels: 0
 DB: 21 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AAZ45827 (1-2088)

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 DB 1117 CCNACNAARNTNTTYGARCNCNACNGARTGYGNAAYGNTAYGTNGARGCNGNGARGAR 1176

QY 21 CysAspCysGlyPheHisValGluCysTYrGlyLeuCySLysLysCysSerLeuSer 40
 DB 1177 TGYGATYGGNTTYCAAGTNGARTGYTAAGNTNTCTGYAARAARTGYWSNTWMSN 1236

QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnPro 60
 DB 1237 AAYGNGCNCAYGTGWSNGAYGNCNCNTGYGAAYAAVACNWSNTGYTNTTYCARCCN 1296

QY 61 ArgGlyTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTYrCysThrGly 80
 DB 1297 MNGSNTAYVARGTGMNGAYGNCNTNAYVARGTGYATTHACGARTATYTAACNGGN 1356

QY 81 AspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTYrAlaCysAsnGlnAsn 100
 DB 1357 GAYWSNGNCARTGYCCNCCNAAAYTNCAYARCARARGAYGNTAYGCTGYAAYCARAY 1416

QY 101 GlnGlyArgCys 104
 DB 1417 CARGNGMNTGY 1428

Search completed: October 21, 2003, 10:34:11
 Job time : 278.138 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:21:31 ; Search time 2467.22 Seconds
(without alignments)
1024.499 Million call updates/sec

Title: US-09-634-252a-4_COPY_496_599
Perfect score: 630
Sequence: 1 PTKLFEPTECNGYVAGEE.....CPNLHKODGYACNONGRC 104

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame+ p2n model -DEV=xlh
O=/cgn2.1/USPTO/US09634252/runat_21102003_090324_3341/app_query.fasta_1.462
-DB=EST -QFMT=fastap -SUFIX=p2n.rst -MINMATCH=0.1 -LOOPL=0 -LOOEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human10.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=lc -MODE=LOCAL
-OUTFMT=plco -NOM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBS=US09634252.gcgn 1.1.3596 @runat_21102003_090324_3341 -NCPU=6 -ICPU=3
-NO MAP -LARGEJURY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_estlum: *
3: em_estlin: *
4: em_estlm: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estlum: *
16: em_estom: *
17: em_gss_hum: *
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19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	728	13	BUS39967
2	614	97.5	470	14	CB733332
3	611	97.0	2891	11	AK046677
4	611	97.0	3433	11	AK029301
5	611	97.0	3498	11	AK034022
6	578	91.7	340	14	F08148
7	563	89.4	722	12	B184544
8	560	88.9	752	10	BF691008
9	541.5	86.0	648	13	BUS36219
10	541.5	86.0	660	13	BUS35688
11	535.5	85.0	661	13	BUS8998
12	526.5	83.6	326	14	R15038
13	517.5	82.1	648	13	BUS31413
14	509	80.8	553	10	AW961362
15	502	79.7	405	14	R52569
16	492.5	78.2	664	12	B1429326
17	485	77.0	261	9	AA317222
18	480.5	76.3	652	12	B1429301
19	479.5	76.1	616	12	B1476560
20	465.5	73.9	598	12	B1981504
21	464	73.7	652	9	AV340595
22	458.5	72.8	599	12	BM070858
23	443.5	70.4	583	12	BM16739
24	438.5	69.6	579	12	B1844587
25	406.5	64.5	513	14	CB716849
26	404.5	64.2	443	14	CB788730
27	404.5	64.2	609	14	CB580769
28	404.5	64.2	704	14	BY722939
29	397	63.0	432	12	B1018895
30	387	61.4	400	14	CB523459
31	385.5	61.2	397	10	AM898896
32	384.5	61.0	618	12	BJ495352
33	378	60.0	402	12	B1019679
34	375	59.5	690	12	BJ059956
35	370.5	58.8	471	14	CB732873
36	344	54.6	428	9	AA718688
37	340.5	54.0	481	13	BY255403
38	338	53.7	552	9	AM660536
39	337	53.5	447	10	BF905823
40	317.5	50.4	622	14	CB578552
41	289.5	46.0	512	12	B1839501
42	287.5	45.6	570	10	BB611717
43	286.5	45.5	546	12	BP009939
44	283	44.9	570	13	BQ833435
45	278.5	44.2	703	14	CB512918

ALIGNMENTS

RESULT 1
BUS39967
LOCUS BUS39967
DEFINITION AGENCOURT 10254064 NIH_MGC_128 Homo sapiens cDNA clone
IMAGE:6570971 5', mRNA sequence.
ACCESSION BUS39967
VERSION BUS39967.1 GI:22850408
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 728)

RESULT 3
AK046677
LOCUS
DEFINITION
2891 bp mRNA linear HTC 05-DEC-2002
Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
metalloprotease domain 23, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK046677.1 GI:26091652
HTC; CAP trapper.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitanai, T., Tushiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishogi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsumoto, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20510913
11076861

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Akiuchi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesci, G.,
Quackenbush, J., Schmitt, L. M., Stebbins, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamita, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Momtaz, P., Nordone, P.,
Ringo, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Tayama, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2891)
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 220-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
URL: http://location/Qualifiers

FEATURES
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BASE COUNT
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ORIGIN
Alignment Scores:
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Score: 611.00 Matches: 100
Percent Similarity: 98.08% Conservative: 2
Best Local Similarity: 96.15% Mismatches: 0
Query Match: 96.98% Indels: 0
DB: 11 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AK046677 (1-2891)

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QY 41 AsnGlyAlaHisCysSerAspGlyProCGsCyAsnAsnThSerCySleuPheGlnPro 60
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QY 61 ArgGlyTYrGluCySArPaPaIaVaIAsnGluCyAspIleThrguTYrGly 80
1978 CGAGGTATATATGTCGGATGCGGATCCGTAAACAGCTGTGATATCCCGAGTACTGCACTGCA 2037

QY 81 AspSerGlyGlnCySProaenLeuHisIsvGlnAspGlyTYrAlaCySAsnGlnAsn 100
|||||

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Db	2098	CAGGCTCCGCTGC 2109	
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DEFINITION	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832416K07 product: a disintegrin and metalloprotease domain 23, full insert sequence.		linear HTC 05-DEC-2002
ACCESSION	AKO29301		
VERSION	AKO29301.1	GI:26081272	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349666		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitaura, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsushita, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aikawa, K., Iwata, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakado, T., Pesole, G., Quackenbush, J., Schriml, L. M., Stabili, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., But, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hochmann, M., Hume, D. A., Kamaya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Matzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weltz, C., Whiteaker, C., Wilmink, L., Wysho-Boris, A., Yoshida, K., Haegawa, Y., Kawai, H., Kontecki, S. and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		
PUBMED	11217651		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		

TITLE
JOURNAL
REFERENCE
AUTHORS

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3433)
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T., Hoti, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohashi, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="PANTOM,DB:4832416K07"
 /db_xref="taxon:10090"
 /c1one="4832416K07"
 /clone_type="head"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="0 day neonate"
 1..3433
 /note="a disintegrin and metalloprotease domain 23 (MGF|MG1:1345162, GB|NM_011780, evidence: BLASTN, 100%, match=2431)"

BASE COUNT 944 a 792 c 836 g 861 t

ORIGIN

Alignment Scores:
 Pred. NO.: 4.68e-51 Length: 3433
 Score: 611.00 Matches: 100
 Percent Similarity: 98.08% Conservative: 2
 Best Local Similarity: 96.15% Mismatches: 2
 Query Match: 96.98% Indels: 0
 Gaps: 0

US-09-634-252A-4_COPY_496_599 (1-104) x AK029301 (1-3433)

QY 1 ProthrlrslsleuphegluprprothrglucysglvAsncllyrrValAGlAlaglyglucl 20

Db 1099 CCAACTAAGCTGTTTGAAGCCACCGAATGTGGAAATGATATGTGGAGCGCGGGAGAGAA 1158

QY 21 CysAspCySglPheHsVAlGluCyTylrGlyLeuCyScySlySLyScySesrLeuSer 40

Db 1159 TGGCACTGTGTGTTCCATGTGGAAATGCTATGGAGTTTGGCTGTGAAGAGTGTTCCTCC 1218

QY 41 AsnclvAlahlsCySesrAspGlyProCyScySAsnAsnthrSerCySleupheglInpro 60

Db 1219 AATGGGGCCCACTGCACTGAGCGGCCCTGCTGTAAACAACCTCATGCTTTTCAGTCA 1278

QY 61 ArgcllyrrGluCySAsrAspAlaValAlaSnclucysAspIlethrGlyrrCySThrGly 80

Db 1279 CGAGGGATGATATCGGATCGCGTAAACAGCTGTATATACACCGAGTACTGCATGCA 1338

Qy 81 Abspserglyncysproproanleuhishysglnaspglytyrcalaicysasn 100

Db 1339 GACCTGTGGCCAGTCCACCCAGCACTCATTAACAAATGCTATGCTGATCAAT 1398

Qy 101 GlnGlyAArgCys 104

Db 1399 CAGGTCGCTGC 1410

RESULT 5

AK034022

LOCUS

DEFINITION Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330142F22 product: a disintegrin and metalloprotease domain 23, full insert sequence.

ACCESSION AK034022

VERSION AK034022.1 GI:26329622

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL MEDLINE 20495374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitanaka, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system-384-format

JOURNAL MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, T., Pesole, G., Queckenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagnier, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Baren, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., But, C., Fletcher, C., Fujita, M., Gariboldi, M., Gusticich, S., Hill, D., Hotmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Matzarrelli, J., Mombauris, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyshew-Borja, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL MEDLINE 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

JOURNAL MEDLINE 420, 563-573 (2002)

PUBMED 12002

REFERENCE 6 (bases 1 to 3498)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL MEDLINE 16-JUL-2001

PUBMED 11009090

REFERENCE 7

AUTHORS

TITLE Submitted (16-JUL-2001) Yoshinide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.

URL: http://genome.gsc.riken.go.jp/

LOCATION: http://fantom.gsc.riken.go.jp/

FEATURES

SOURCE

1. 3498

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="PANTOM_DB:9330142F22"

/db_xref="taxon:10090"

/clone="9330142F22"

/sex="male"

/tissue_type="dienecephalon"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

303. 2375

/note="unnamed protein product: a disintegrin and metalloprotease domain 23 (MGI:1345162, GBNM_011780, evidence: BLASTN, 100%, match=2431)

putative"

/codon_start=1

/protein_id="BAC28550.1"

/db_xref="GI:26329622"

/translation="MKPRGIISSRRSLTSGSCTFGCGRCSPGPPAPAPRCILLVLLPLALTSRRPRRGAAPSPAHNNETRAETLGLVLADEDTLQONSSRTSYSAVKEETLPSRLVLYINODESPYHVLDTARIQKRNKVAQAQFOLEAFSGKFLIDTLNUNGSLSSRYVEIHYEDGKQMSGCEHYOSIGVDSRVALSTCNGLHMFEDDTFVYMEPELTDEKSTGRPHIIQTLGQYSKOMKNDSTDSDDWPLLEIQMLRRKRAVNSPGLVEPEMEYLEMTIINDHRTYKRHS SHAHTNNPFAKSVNLVDSIYKEDLNRYLVAVETWETREKXIDITINPNOMLDFSRRIORIOHDAVHLISVTFH YKSSLSYFEGVCVRIRGVVNEGYCLPMAYQVLSQSLAONLGIOMEPPSRKPCCEI ESNGKCMETGTGVSHSKRFKCSILEFRDVLQGGGACLPNRPKLFEPEPCGNGVE AGECDGDFGVEYVCEYVCKKCSLNGHCDGCGCNNTSCLFQSRGECDAVNSCDI TEYCTGGCCGCPNLHKGDSYSCNONGRCYVNECEKTRQDCQYIWTKAAGDAPFCY EKATNTEETKGNCGKDDRWIPCSKIDVFCGFLCTLVLTAPRIGLQGEIIPSPFVH QGVINDR"

BASE COUNT 906 a 880 c 853 g 859 t

ORIGIN

Alignment Scores:

Pred. No.: 4,79e-51 Length: 3498
Score: 611.00 Matches: 100
Percent Similarity: 98.08% Conservative: 2
Best Local Similarity: 96.15% Mismatches: 2
Query Match: 96.98% Indels: 0
DB: 11 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x AK034022 (1-3498)

QY 1 ProthylveleuphegluProthrgluCysGlyAsnGlyTyrValGluAlaGlyGluGlu 20
DB 1779 CCACTAAAGCTGTTGAGCCCAAGGATGTGAAAGATGTGAGAGCCGAGGAGGAA 1838
QY 21 CysAspCysGlyPheHisValGluCysTyrGlyLeuCySlySlySlySlySerLeuSer 40
DB 1839 TCCGACTGCTGTTCCATGATGCAATGCTTGAAGTTGCTGTAAGAAGCTTCCTCC 1898
QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuphegluPro 60
DB 1899 AATGGGGCCCACTGACAGTACGGCCCTGCTGTAAACACACCTCATGCTTTTTCAGTCA 1958
QY 61 ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGly 80
DB 1959 CGAGGCTATGAATGTGGGATGCCGTAAACAGCTGTATACCCAGTACTGCTGCA 2018
QY 81 AspSerGlyGlnCysProProAsnLeuHislySlyGlnAspGlyTyrAlaCysAsnGlnAsn 100
DB 2019 GACTCTGGCCAGTCCCACTGCAACCTCCATTAAACAGATGGCTATAGCTGCATCAAAAT 2078
QY 101 GlnGlyArgCys 104
DB 2079 CAGGCTCGCTGC 2090
RESULT 6
F08148
LOCUS F08148 340 bp mRNA linear EST 21-FEB-1995
DEFINITION HSCRF011 normalized infant brain cDNA Homo sapiens cDNA clone
ACCESSION F08148
VERSION F08148.1 GI:677656
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 340)
AUTHORS Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastien, Kabakchis, C. and Tessier, A.
TITLE IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
PUBMED 7757816
COMMENT Contact: Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 Evry Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genethon@genethon.fr
Single read
Genethon library_id: C; Genethon_sequence_id: y1c-21f01
Seq primer: (-21)M13_universal.
Location/Qualifiers
1..340
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C-21f01"
/sex="Female"

/tissue_type="total brain"
/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lambda B; Site: 1: HindIII;
Site 2: NotI; sex=Female; dev_stage=3 months old;
Isolate=muscular atrophy patient; tissue_type=total brain
; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lambda B vector. Clone library from B.Scores, Psychiatry
Dept. Columbia University, USA
Bento Scores, P.N.A.S in press"
BASE COUNT 87 a 70 c 90 g 84 t 9 others
ORIGIN

Alignment Scores:

Pred. No.: 5.09e-49 Length: 340
Score: 578.00 Matches: 97
Percent Similarity: 94.17% Conservative: 0
Best Local Similarity: 94.17% Mismatches: 6
Query Match: 91.75% Indels: 0
DB: 14 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x F08148 (1-340)

QY 2 ThrlySleuphegluProthrgluCysGlyAsnGlyTyrValGluAlaGlyGluGluCys 21
DB 27 ACAAGCTATTATTNACCCAGCAAGATGTGAATGNTGCGAAGCTGGGAGAGTGT 86
QY 22 AspCysGlyPheHisValGluCysTyrGlyLeuCySlySlySlySlySerLeuSerAsn 41
DB 87 NATGTGTTTATGATGGAATGCTATGATATTATCTAAGAAATGTCCTCCAC 146
QY 42 GlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuphegluProArg 61
DB 147 GGGGCTCACTGACGAGGAGGGCCCTGCTGTAACTACTCATGCTTTTTCAGCAGCA 206
QY 62 GlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGlyAsp 81
DB 207 GGGTATGAATGCGGAGATGCTGTGAACAGATGTATTAAGTAATATTGTAAGTGAAC 266
QY 82 SerGlyGlnCysProProAsnLeuHislySlyGlnAspGlyTyrAlaCysAsnGlnAsn 101
DB 267 TCTGTGATGAGTCCCACTGCAACCTTCATTAAGCAAGCGATATGATCAATCAAAATCAG 326
QY 102 GlyArgCys 104
DB 327 GGGCCCTGC 335
RESULT 7
B1184544
LOCUS B1184544 722 bp mRNA linear EST 10-JUL-2001
DEFINITION UNL-P-FN-co-e-05-0-UNL_61 UNL-P-FN Sus scrofa cDNA clone
ACCESSION UNL-P-FN-co-e-05-0-UNL_61
VERSION B1184544.1 GI:14658953
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 722)
AUTHORS Caetano, A.R., Johnson, R.K. and Pomp, D.
TITLE Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles
JOURNAL Mamm. Genome 14 (1), 65-70 (2003)
MEDLINE 22419904
PUBMED 12532269
COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362

Email: dpomp@unl.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The following repetitive elements were found in this cDNA sequence: 3-43, >(TAAA)n\$Simple_repeat
Seq primer: M13 -29
POLYA=yes.

FEATURES
source

```
1. 722
   Location/Qualifiers
   /organism="Sus scrofa"
   /mol_type="mRNA"
   /strain="University of Nebraska, Lincoln Swine Selection
   lines"
   /db_xref="taxon:9823"
   /clone="UNL-P-FN-co-e-05-0-UNL"
   /dev_stage="ADULT"
   /lab_host="DH10B (Life Technologies)"
   /clone_lib="UNL-P-FN"
   /note="Vector: pTZ19-Pac (Pharmacia) with a modified
   polylinker. Site 1: Not I; Site 2: Eco RI; The UNL-P-FN
   library is a normalized library representing porcine
   ovarian follicles, ranging between 2.0 to 10.0 mm in
   diameter, collected during 7 days of the follicular phase
   of the pig estrous cycle. This library was derived from
   the library UNL-P-F2. The tag is a string of 5-6
   nucleotides present between the Not I site and the
   oligo-dT track. The library was constructed as described
   by Bonaldo, Lennon and Soares, Genoms Research 6: 791-806
   , 1996.
   TAG_SEQ=None found"
```

BASE COUNT 188 a 181 c 131 g 222 t

ORIGIN

Alignment Scores:

Pred. No.: 4.46e-47 Length: 722
Score: 563.00 Matches: 92
Percent Similarity: 97.89% Conservative: 1
Best Local Similarity: 96.84% Mismatches: 2
Query Match: 89.37% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x B1184544 (1-722)

```
OY 10 CysGlyAsnGlyTyrValGluAlaGlyGluGluCysAspCysGlyPheHisValGluCys 29
Db 721 TGTGAAACGGCTTATCTGAGAGCTGGAGGAGATCGATGGGATTCATGTTGGAATGC 662
OY 30 TyrGlyLeuCySylAsylCysSerLeuSerAsnGlyAlaHisCysSerAspGlyPro 49
Db 661 TACGACACTGCTGCAAGAAATGCTCTCTCTCAACGGATGCCCATTTGACAGCGAGGCC 602
OY 50 CysCysAsnAsnThrSerCysLeuPheGlnProArgGlyTyrGlyCysArgAspAlaVal 69
Db 601 TGCCTTAATAGTACTGCTCTTTTTCAGCCACCTGGGTATGATGTCGGGATCTCTGTG 542
OY 70 AsnGlyCysAspGlyLeuThrGlyTyrCysThrGlyAspSerGlyGlnCysProProAsnLeu 89
Db 541 AATGATGATGATATTAACCGAATATTTACTGAGAGCTGCGCACATGCCCAAAATCTT 482
OY 90 HisLysGlnAspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCys 104
Db 481 CATAGCAAGATGTTATGATGCAATCAAAATCAGGCCCGCTGC 437
```

RESULT 8
BF691008 752 bp mRNA linear EST 22-DEC-2000
LOCUS 602247043F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332275 5',
DEFINITION mRNA sequence.
ACCESSION BF691008
VERSION BF691008.1 GI:11976416
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 752)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rcs@bbs-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM198 row: e column: 12
High quality sequence stop: 719.

FEATURES
source

```
1. 752
   Location/Qualifiers
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:4332275"
   /tissue_type="melanotic melanoma, high MDR"
   /lab_host="DH10B (TI phase-resistant)"
   /clone_lib="NIH MGC 62"
   /note="Organ: skin; Vector: pNNR-LIB (Clontech); Site 1:  
SfiI (ggccgagcggcc); Site 2: SfiI (ggccatcatggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CACGGCATTTAGGCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGCGAGCGGCCGATG-dt(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."
```

BASE COUNT 195 a 151 c 217 g 189 t

ORIGIN

Alignment Scores:

Pred. No.: 9.46e-47 Length: 752
Score: 560.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.89% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x BF691008 (1-752)

```
OY 13 GlyTyrValGluAlaGlyGluGluCysAspCysGlyPheHisValGluCysTyrGlyLeu 32
Db 1 GGATACGTGGAAGCTGGGAGAGTGTATGTTGTTTCAATGGAATGCTATGATGA 60
OY 33 CysCysLysCysCysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsn 52
Db 61 TGCCTTAAGAAATTTCCCTCTCCACCGGCGCTACTGACGACGCGGCCCTGCTGTAAC 120
OY 53 AsnThrSerCysLeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCys 72
Db 121 AATACCTCATGCTCTTTTTCAGCCACGAGGATGATGATGCGGATGCTGTGAAGAGT 180
OY 73 AspIleThrGlyTyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGln 92
Db 181 GATATTACTGATATTTTACTGAGAGCTGCTGAGTCCACAAATCTTTCATTAACCA 240
OY 93 AspGlyTyrAlaCysAsnGlnAsnGlnGlyArgCys 104
Db 241 GACGATATGATGATCAATCAAAATCAGGCCCGCTGC 276
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RESULT 9
BU396219

LOCUS BU396219 648 bp mRNA linear EST 27-NOV-2002
 DEFINITION 603805442F1 CSEQCHN57 Gallus gallus cDNA clone CHEST783d12 5', mRNA
 ACCESSION BU396219
 VERSION BU396219.1 GI:25765275
 KEYWORDS EST
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 648)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken CDNAS
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..648
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST783d12"
 /dev_stage="16 day embryo"
 /lab_host="DH10B"
 /clone_11b="CSEQCHN57"
 /note="Organ: Brain; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."
 BASE COUNT 187 a 117 c 169 g 175 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,81e-45 Length: 648
 Score: 541.50 Matches: 91
 Percent Similarity: 91.35% Conservative: 91
 Best Local Similarity: 87.50% Mismatches: 8
 Query Match: 85.95% Indels: 1
 DB: 13 Gaps: 1
 US-09-634-252A-4_COPY_496_599 (1-104) x BU396219 (1-648)
 QY 1 ProtrlyleuPhegujProthrguCySGlyAsnglyrVaigluaglyguu 20
 DB 228 CCAACAAAGCTCTTCAACTAGTGTGGAATGATGTAGACACAGAGAGAGA 287
 QY 21 CysaspCySgLyPhehisValGluCyTYrGlyLeuCyCySylslyScysSerleuser 40
 DB 288 TCGGATGGCGTTTCCGATGGAATGCTACGACGACTGTGTAGAGAGGCTCTTTT 347
 QY 41 AenglyAlahicysSerhsnglyProCyCySasnaSrthSerCySleuPheguInPo 60

DB 348 AATGAGCTCACTGATGATGGCCCTGCT---AATAGCTGCTGCTTTTTTTCGA 404
 QY 61 ArgGlyTYrGluCyAsrGAlaValAsnglyuCySAspIlethrglyTyCySthrcly 80
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 QY 81 AspSerGlyGlnCySProPAsnleuhtlsySglnaPglTYrAlaCySasnglnaSn 100
 DB 465 GATTTCGCCAGATGTCACCAATATCTCATTAACAAGATGATATGCTTGATTTCTAAT 524
 QY 101 GInGlyArGcyG 104
 DB 525 CAGGACCGCTGC 536
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 DEFINITION 603805095F1 CSEQCHN57 Gallus gallus cDNA clone CHEST782n24 5', mRNA
 ACCESSION BU395688
 VERSION BU395688.1 GI:25764744
 KEYWORDS EST
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 660)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken CDNAS
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /db_xref="taxon:9031"
 /clone="CHEST782n24"
 /dev_stage="16 day embryo"
 /lab_host="DH10B"
 /clone_11b="CSEQCHN57"
 /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
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 BASE COUNT 193 a 122 c 170 g 174 t
 ORIGIN
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 Mismatches: 8
 Indels: 1
 Gaps: 1

US-09-634-252A-4_COPY_496_599 (1-104) X BU395688 (1-660)

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QY	21	CysAspCysGlyPheHisValGluCysTyrGlyLeuCysCysLysLysCysSerLeuSer	40
DB	301	TGCGATTGCGGTTCCGAATGGAATGCTACCGCAGACTGTGTAAAAAGTGCTCTTTCT	360
QY	41	AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnPro	60
DB	361	AATGAGCTCTCACTGTAGATGATGGGCTTGCTGT--AATAGTGTGTCTTTTTCCTCA	417
QY	61	ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGly	80
DB	418	CGAGGCTATGACTGTAGATATGACAGTGAATGATGTGATATTGCAGATTCTGCACGTGA	477
QY	81	AspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsn	100
DB	478	GATTCTGGCCAGTGTCCACCAATCTTCATTAACAAGATGATATGCTTGATTTCTAAT	537
QY	101	GlnGlyArgCys	104
DB	538	CAGGAGCGTTGC	549

Search completed: October 21, 2003, 13:06:54
 Job time : 2478.22 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: October 21, 2003, 10:12:31 ; Search time 1815.35 Seconds
(without alignment)
1239.449 Million cell updates/sec

Title: US-09-634-252A-4_COPY_532_586
Perfect score: 332
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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36: em_hcg_mam:*
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41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	332	100.0	1668	6 AX235014	AX235014 Sequence
2	332	100.0	2499	6 BD130423	BD130423 DNAs and
3	332	100.0	3054	6 E26532	E26532 Novel prote
4	332	100.0	3054	9 AB009672	AB009672 Homo sapi
5	332	100.0	3079	9 HSA5580	AJ005580 Homo sapi
6	332	100.0	4043	6 AX299710	AX299710 Sequence
7	319	96.1	2891	10 AB009673	AB009673 Mus muscu
8	213	64.2	1464	6 E10490	E10490 CDNA encodi
9	213	64.2	1464	6 E125845	E125845 Sequence 5
10	213	64.2	1464	6 E13482	E13482 Sequence 5
11	213	64.2	2908	6 H10492	D17390 Homo sapien
12	213	64.2	2913	6 E10492	E10492 CDNA encodi
13	213	64.2	2913	6 E125847	E125847 Sequence 7
14	213	64.2	2913	6 E13484	E13484 Sequence 7
15	213	64.2	2923	6 E10491	E10491 CDNA encodi
16	213	64.2	2923	6 E125846	E125846 Sequence 6
17	213	64.2	2923	6 E13483	E13483 Sequence 6
18	213	64.2	3168	6 AB009675	AB009675 Homo sapi
19	213	64.2	3183	6 E10493	E10493 CDNA encodi
20	213	64.2	3183	6 E125848	E125848 Sequence 8
21	213	64.2	3183	6 E13485	E13485 Sequence 8
22	213	64.2	3229	10 AB009676	AB009676 Mus muscu
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24	185	55.7	1674	6 AX235012	AX235012 Sequence
25	185	55.7	2604	6 BD130424	BD130424 DNAs and
26	185	55.7	2697	6 E26531	E26531 Novel prote
27	185	55.7	2786	9 AB009671	AB009671 Homo sapi
28	185	55.7	2796	9 AF155381	AF155381 Homo sapi
29	185	55.7	2805	6 E26530	E26530 Novel prote
30	185	55.7	2858	9 AF155382	AF155382 Homo sapi
31	185	55.7	3259	9 AF158637	AF158637 Homo sapi
32	185	55.7	3295	9 AF073291	AF073291 Homo sapi
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34	183	55.1	3447	5 AF032383	AF032383 Xenopus l
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38	168.5	50.8	276	6 AX698112	AX698112 Sequence
39	168.5	50.8	1638	6 AX235004	AX235004 Sequence
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41	168.5	50.8	2720	9 HSU46005	U46005 Human MDC15
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ALIGNMENTS

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LOCUS AX235014 1668 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 17 from Patent WO0162905.
ACCESSION AX235014
VERSION AX235014.1 GI:15593673
KEYWORDS
SOURCE
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Fanelow, W.C., Cerretti, D.P., Poindexter, K.M. and Black, R.A.
Integrin antagonists
Patent: WO 0162905-A 17 30-AUG-2001;
IMMUNEX CORPORATION (US)
LOCATION/Qualifiers
1. 1668
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
DB 232 CTTTTCAGCCACGAGGGATGATGATGCCGGAGATGCTGTAAAGAGTGTATTAATCTGAA 291
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
DB 232 TATTGTACTGAGACTCTGGTCAGTGCCACCAAAATCTTCATTAAG 336
RESULT 2
BD130423 2499 bp DNA linear PAT 18-SEP-2002
LOCUS BD130423
DEFINITION DNAs and polypeptides of metalloprotease disintegrins SVPH3-13 and
SVPH3-17.
ACCESSION BD130423
VERSION BD130423.1 GI:223225368
KEYWORDS JP 2002503472-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 2499)
AUTHORS Cerretti, D.P.
TITLE DNAs and polypeptides of metalloprotease disintegrins SVPH3-13 and
SVPH3-17
JOURNAL Patent: JP 2002503472-A 2 05-FEB-2002;
IMMUNEX CORP
OS Homo sapiens (human)
PN JP 2002503472-A/2
PD 05-FEB-2002
PF 11-FEB-1999 JP 2000531569
PI 11-FEB-1998 US 60/074310
PC DOUGLAS PAT CERRETTI
PC C12N15/09, C07K16/40, C12N1/19, C12N1/21, C12N5/10, C12N9/64 PC
, C12O1/37, G01N33/68
PC C12N15/00, C12N5/00
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QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
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DB 1714 TATTGTACTGAGACTCTGGTCAGTGCCACCAAAATCTTCATTAAG 1758
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E26532 3054 bp DNA linear PAT 18-JUN-2001
LOCUS E26532
DEFINITION Novel protein belonging to MDC gene family and DNA encoding the
same.
ACCESSION E26532.1 GI:13026199
VERSION E26532
KEYWORDS JP 1999155574-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 3054)
AUTHORS Koji, S.
TITLE Novel protein belonging to MDC gene family and DNA encoding the
same
JOURNAL Patent: JP 1999155574-A 3 15-JUN-1999;
EIGAI CO LTD
OS Homo sapiens (human)
PN JP 1999155574-A/3
PD 15-JUN-1999
PR 01-DEC-1997 JP 1997330020
PR

PI KOJI SONE
PC C12N15/09, C07K14/47, C07K16/18, C12N1/21, C12P21/02, C12Q1/68// PC
(C12N15/09, C12R1.91), (C12N1/21, C12R1.19), (C12P21/02, C12R1.19), PC
C12N15/00,
PC (C12N15/00, C12R1.91)
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CC Topology: Linear;
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FT CDS 224..2719.
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Query Match: 100.00% Indels: 0
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Db 1877 CTTTTCAGCCACGAGGATGATGATGCGGGATGCTGTGAACGATGTGATATTACTGAA 1936
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Db 1937 TATTGTACTGAGACTGTGTGATGCGCCACCAATCTTCATTAAG 1981
RESULT 4
AB009672 3054 bp mRNA linear PRI 15-AUG-1998
LOCUS Homo sapiens mRNA for MDC3, complete cds.
DEFINITION
ACCESSION AB009672.1 GI:3419877
VERSION
KEYWORDS MDC3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Sagane, K., Ohya, Y., Hasegawa, Y. and Tanaka, I.
TITLE Metalloprotease-like, disintegrin-like, cysteine-rich proteins
MDC2 and MDC3: novel human cellular disintegrins highly expressed
in the brain
JOURNAL Biochem. J. 334 (Pt 1), 93-98 (1998)
MEDLINE 98359734
PUBMED 9633107
2 (bases 1 to 3054)
Sagane, K.
REFERENCE Direct Submission
TITLE Submitted (11-DEC-1997) Koji Sagane, Eisai Co., Ltd., Tsukuba
JOURNAL Research Laboratories; Tokodai 5-1-3, Tsukuba, Ibaraki 300-2635,
Japan (E-mail: k1-sagane@eisai.co.jp, Tel: +81-298-47-5813,
Fax: +81-298-47-5367)
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Best Local Similarity: 100.00% Mismatches: 0
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QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValangluCysAspIleThrGlu 40
Db 1877 CTTTTCAGCCACGAGGATGATGATGCGGGATGCTGTGAACGATGTGATATTACTGAA 1936
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
Db 1937 TATTGTACTGAGACTGTGTGATGCGCCACCAATCTTCATTAAG 1981
RESULT 5
HSAS580 3079 bp mRNA linear PRI 18-JAN-2001
LOCUS Homo sapiens mRNA for adam23 protein.
DEFINITION
ACCESSION AU005580.1 GI:12053562
VERSION adam23 gene; Adam23 protein; disintegrin; metalloprotease.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Cal, S. and Lopez-Otin, C.
TITLE Identification and characterization of ADAM 23, a novel
metalloprotease/disintegrin protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3078)
AUTHORS Lopez-Otin, C.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo, C/ Julian Claveria 6. Oviedo.
Asturias., 33006, SPAIN
REMARK revised by author 23-APR-1998, revised by author 26-OCT-1998
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KFLDILLNGLSSDVEIHYENKGPQSKGEHCYHGSIRGVKDSVALSTCNGL
HMFEDDIFVVMIEPLVHDEKSTGRPHIIOKTLGAGYKQMKMLTMRGQMPFLS
ELQMKLRRAVNSPGRGPEEMKYLELMTVNDHTYKGRSSHAHTNPAKSVNLVD
STYKQOLNRVVLVAVTWTEKDOIITITNPVOMLHPSKYRORTKQADAVHLISRV
TTHYKRSLSITFGVCYSRTGCVNBYGLPAAVAVLSQSLQNLGIQWEPSSRKPIC
DCTESWGCGIMEETGVSHSRKFSKCSILEYRDFLQRGGACLFRNPFLFEPTGNG
VYAGEBCDCGFHVECYGLCKKCSLSNGHSCSDGPCNNNTSCLPQPGYECRDVNE
CDITEYCTGDSGQCPNLHAKQDYACNQGRCYNGECKTRDMCCOYIWTGTAAGSDK
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FYHOGRVLDCCGAHVLDLDDTDVYEDGTGCGSMCLDRKCIQIOLNMSCTDS
KGRVSGHVCSENEATCTCTFTWAGTDCIRDPVRNLHPKDEGRGSPATNLIIGSI
AGAILVAALVLDGTGWFKNVKKRRFPDQGPPI"
BASE COUNT 865 a 714 c 769 g 731 t
ORIGIN
3'UTR
/gene="adam23"
Alignment Scores:
Pred. No.: 1,13e-30 Length: 3079
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-634-252A-4_COPY_532_586 (1-55) x HSA5580 (1-3079)
QY 1 CysSerLeuSerArgGlyAlaHisCysSerArgGlyProCysCysAsnAsnThrSerCys 20
Db 1646 TTTTCCCTCTCCACAGGGGCTCAGTCAGCAGCGGGCCCTCTGTAACAATACCTCATGT 1705
QY 21 LeuphegInProArgGlyTyrGluCysArgAspAlaValaAngluCysAspIleThrglu 40
Db 1706 CTTTTCAGCCACAGAGGATGATGATCCGGATGCTGTGAAGAGATGATTTACTGA 1765
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1766 TATTGTACTGAGAGACTGTGTGAGTCCACCAAAATCTTCATTAAG 1810
RESULT 6
LOCUS AX299710 4043 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 2 from Patent WO0174857.
ACCESSION AX299710
VERSION AX299710.1 GI:17129252
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lopez-Otin,C., Freilij,J.M., Bianchi,A.B., Mguel,S.C., Garcia,J.M.
TITLE Methods and compositions for modulating integrin-mediated cell-cell
interactions
JOURNAL Patent: WO 0174857-A 2 11-OCT-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
LOCATION/Qualifiers
SOURCE 1..4043
/organism="Homo sapiens"
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/mol_type="genomic DNA"
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BASE COUNT 1110 a 946 c 1002 g 985 t
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Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-634-252A-4_COPY_532_586 (1-55) x AX299710 (1-4043)
QY 1 CysSerLeuSerArgGlyAlaHisCysSerArgGlyProCysCysAsnAsnThrSerCys 20
Db 2610 TTTTCCCTCTCCACAGGGGCTCAGTCAGCAGCGGGCCCTCTGTAACAATACCTCATGT 2669
QY 21 LeuphegInProArgGlyTyrGluCysArgAspAlaValaAngluCysAspIleThrglu 40
Db 2670 CTTTTCAGCCACAGAGGATGATGATCCGGATGCTGTGAAGAGATGATTTACTGA 2729
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 2730 TATTGTACTGAGAGACTGTGTGAGTCCACCAAAATCTTCATTAAG 2774
RESULT 7
LOCUS AB009673 2891 bp mRNA linear ROD 17-AUG-1999
DEFINITION Mus musculus mRNA for ADAM23, complete cds.
ACCESSION AB009673
VERSION AB009673.1 GI:5736618
KEYWORDS ADAM23.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Sagane,K., Yamazaki,K., Mizui,Y. and Tanaka,I.
TITLE Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23
JOURNAL Gene 236 (1), 79-86 (1999)
MEDLINE 99365303
PUBMED 10433968
REFERENCE 2 (bases 1 to 2891)
AUTHORS Sagane,K.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-1997) Koji Sagane, Eisai Co., Ltd., Tsukuba
Research Laboratories; Tokodai 5-1-3, Tsukuba, Ibaraki 300-2635,
Japan (E-mail:k-sagane@hcc.eisai.co.jp, Tel:+81-298-47-5813,
Fax:+81-298-47-5367)
COMMENT Sequence updated (07-Aug-1999).
FEATURES
LOCATION/Qualifiers
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/organism="Mus musculus"
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LDLILNGLSSDVEIHYEDGKQYKSGGHCYHGSIRGVKDSVALSTCNGLHGM
FEDDTFVVMIEPLTDEKSTGRPHIIOKTLGAGYKQMKMLTMRGQMPFLPEIQ
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YKRSLSITFGVCYSRTGCVNBYGLPMAVAVLSQSLQNLGIQWEPSSRKPICCECI
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AGBCDCGFHVECYGCKKCSLSNGHSCSDGPCNNNTSCLPQPGYECRDVANS CDI
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QGRVDCGAGVHVDLDDTGVGDEGTGCGSPMLLRKCLQIOLNMSGCPDLSRGK
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ILVAIVLGGTGMGRKXVKRRFDPDPOGPI"
polyA_site
1295

BASE COUNT 763 a 747 c 763 g 618 t
ORIGIN

Alignment Scores:

Pred. No.: 4,1e-29 Length: 2891
Score: 319.00 Matches: 53
Percent Similarity: 96.36% Conservative: 0
Best Local Similarity: 96.36% Mismatches: 2
Query Match: 96.08% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x AB009673 (1-2891)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCyAsnAsnThSerCys 20

DB 1664 TGTTCGCTCTCCAAATGGGCGCCACTGCACTGCGGCCCCCTGCTGTAACAACCTCATGT 1723

QY 21 LeupheginProArxGlyTyrGluCysArxAspAlaValAsnGluCysAspIleThxGlu 40

DB 1724 CTTTTCAGTACGAGGGGTATGATGTCGGGATGCCGTAAACAGCTGTGATATCACCGAG 1783

QY 41 TyrCysThrxGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

DB 1784 TACTGCACTGAGAGACTGTGGCCAGTCCACCAACCTTCATMAA 1328

RESULT 8

E10490 1464 bp RNA linear PAT 29-SEP-1997

LOCUS E10490

DEFINITION cDNA encoding a consensus region of MDC protein.

ACCESSION E10490.1 GI:22027323

VERSION JP 1995330799-A/1.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS Nakamura, Y. and Emi, M.

TITLE MDC PROTEIN AND DNA CODING THE SAME

JOURNAL Patent: JP 1995330799-A 1 19-DEC-1995;

COMMENT JAPAN FOUND CANCER RES, EISAI CO LTD

OS Homo sapiens (human)

PN JP 1995330799-A/1

PD 19-DEC-1995

PR 22-APR-1994 JP 1994084470

PR 14-MAY-1993 JP 93P 136602, 22-SEP-1993 JP 93P 257455, PR

23-FEB-1994 JP 94P 49904, 12-APR-1994 JP 94P 73328 PI

NAKAMURA YUSUKE, EMI MITSURU

PC C07K16/32, C07K14/82, C12N1/21, C12N15/02, C12N15/09, C12P21/02, PC

C12P21/08, C12P21/08, G01N33/53, G01N33/574, (C12N1/21, C12N1:19), (C12N15/09,

PC C12R1:91), (C12P21/02, C12R1:19), (C12P21/08, C12R1:91);

CC etrandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

FH key Location/Qualifiers

FT source 1.1464

FT /organism='Homo sapiens'.

FT /tissue type='Cerebellum'.

FT <1..>1464

FT CDS /product='MDC protein'.

FEATURES location/Qualifiers

source 1.1464

/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

BASE COUNT 294 a 445 c 473 g 252 t
ORIGIN

Alignment Scores:

Pred. No.: 1.87e-16 Length: 1464
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 6 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x E10490 (1-1464)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCyAsnAsnThSerCys 20

DB 1111 TGCACCCGACTCAGCAGCCCATGTGCGACGCGGCTCTGCGCCG-----TGC 1164

QY 21 LeupheginProArxGlyTyrGluCysArxAspAlaValAsnGluCysAspIleThxGlu 40

DB 1165 AAGTACGACACCGGGGTGTCTCTGCGAGAGCGCTGAACGAGTGGACATCGCGAG 1224

QY 41 TyrCysThrxGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

DB 1225 ACGTCACCGGGGACTGTACGACAGTGGCCGCTTAACCTGCACAG 1269

RESULT 9

E125845 1464 bp DNA linear PAT 07-OCT-1996

LOCUS E125845

DEFINITION Sequence 5 from patent US 5552526.

ACCESSION E125845

VERSION I25845.1 GI:1605715

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS Nakamura, Y. and Emi, M.

TITLE MDC proteins and DNAs encoding the same

JOURNAL Patent: US 5552526-A 5 03-SEP-1996;

FEATURES location/Qualifiers

source 1.1464

BASE COUNT 294 a 445 c 473 g 252 t

ORIGIN

Alignment Scores:

Pred. No.: 1.87e-16 Length: 1464
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 6 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x I25845 (1-1464)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCyAsnAsnThSerCys 20

DB 1111 TGCACCCGACTCAGCAGCCCATGTGCGACGCGGCTCTGCGCCG-----TGC 1164

QY 21 LeupheginProArxGlyTyrGluCysArxAspAlaValAsnGluCysAspIleThxGlu 40

DB 1165 AAGTACGACACCGGGGTGTCTCTGCGAGAGCGCTGAACGAGTGGACATCGCGAG 1224

QY 41 TyrCysThrxGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

DB 1225 ACGTCACCGGGGACTGTACGACAGTGGCCGCTTAACCTGCACAG 1269

RESULT 10

LOCUS E125845 1464 bp DNA linear PAT 07-OCT-1996

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DEFINITION      Sequence 5 from patent US 5631351.
ACCESSION       I43482
VERSION         I43482.1  GI:2468726
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 1464)
AUTHORS        Nakamura, Y. and Emi, M.
TITLE           Antibodies to MDC proteins
JOURNAL         Patent: US 5631351-A 5 20-MAY-1997;
FEATURES        Location/Qualifiers
                 source          1..1464
                               /organism="unknown"
BASE COUNT      294 a 445 c 473 g 252 t
ORIGIN
Alignment Scores:
Pred. No.:      1.87e-16      Length:      1464
Score:          213.00        Matches:      36
Percent Similarity: 76.36%    Conservative: 6
Best Local Similarity: 65.45% Mismatches:    11
Query Match:    64.16%       Indels:        2
DB:             Gaps:        1

US-09-634-252a-4_COPY_532_586 (1-55) x I43482 (1-1464)
QY      1  CYSerLeuSerAnGlyAlaHisCYSerAspGlyProCYsCYsAsnAnthrSerCys 20
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1111 TGCACCTTACTACACAGCCATGTGCAGGAGCGGCTCTGCTGTGCCGCC-----TGC 1164

QY      21  LeupheGlnProArgGlyTyrGluCySarGAspAlaValAsnGluCYsAspIleThrGlu 40
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1165 AAGTAGAAGACCAAGGGGTGTGTCTGCTGCCGAGAGCCGTGACGAGTGCACATCGCGGAG 1224

QY      41  TyrCYsThrGlyAspSerGlyGlnCYsProProAsnLeuHisLys 55
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1225 ACCTGCACCGGGACTCTAGCCAGTGCCTCCGCTTAACCTGCACAG 1269
    
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Search completed: October 21, 2003, 12:02:01
 Job time : 1821.35 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: October 21, 2003, 10:11:41 ; Search time 142.862 Seconds

(without alignments)
1039.251 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586

Perfect score: 332

Sequence: 1 CSLSNGAHCSDBGCCNNTSC.....CDITEYCTGDSGQCPNLMHK 55

Scoring table:

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosome2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	332	100.0	1668	22	AA021439	ADAM-23dis-Fc fusi
2	332	100.0	2268	21	AA245826	DNA encoding a dis
3	332	100.0	2268	22	AA511991	Human CDNA encodin
4	332	100.0	2268	24	AB078447	Nucleotide sequenc
5	332	100.0	2499	20	AA210207	CDNA encoding the
6	332	100.0	3054	20	AA278438	Human MDC3 CDNA.
7	332	100.0	3054	25	ABX76201	Lung cancer-associ
8	332	100.0	3054	25	ABX76202	Lung cancer-associ
9	332	100.0	4043	21	AA172025	ADAM 23 CDNA. Hom
10	285	85.8	2088	21	AA245827	Degenerate DNA enc
11	285	85.8	2088	22	AA511992	Human degenerate D
12	285	85.8	2088	24	AB078448	Degenerate nucleot
13	213	64.2	1464	16	AA076119	Human fetal cerebe
14	213	64.2	2923	16	AA076121	Human fetal cerebe
15	213	64.2	2923	16	AA076120	Human fetal cerebe
16	213	64.2	3183	16	AA076122	Human fetal brain
17	185	55.7	1674	22	AA021438	ADAM-22dis-Fc fusi
18	185	55.7	2604	22	AA210208	CDNA encoding the
19	185	55.7	2697	20	AA278437	Human MDC2-beta cD
20	185	55.7	2805	20	AA278436	Human MDC2-alpha c
21	173.5	52.3	2653	17	AA174616	CRII-7 nerve prote
22	168.5	50.8	276	25	AB268583	Nucleotide sequenc
23	168.5	50.8	1638	22	AA021434	ADAM-15dis-Fc fusi
24	168.5	50.8	2720	24	AB235318	Human gene express
25	168.5	50.8	2740	24	AB235317	Human gene express
26	168.5	50.8	2740	24	AB077748	Breast cancer-asso
27	168.5	50.8	2740	24	AB077748	Gene #3360 used to
28	168.5	50.8	2968	22	AA514756	Human protease cDN
29	168.5	50.8	2968	24	AB414523	Human metallopept
30	167	50.3	1500	21	AA459303	DNA encoding a sna
31	167	50.3	2346	21	AA459236	DNA encoding a sna
32	167	50.3	2373	21	AA459236	CDNA encoding a hu
33	167	50.3	2373	21	AA459236	DNA encoding a sna
34	167	50.3	2695	22	AA521345	Human cDNA sequenc
35	167	50.3	2695	25	ACA03704	CDNA encoding huma
36	167	50.3	2695	25	ACA04125	Human cDNA encodi
37	167	50.3	2695	25	ABX89242	DNA encoding novel
38	162	48.8	2058	23	AB141903	Drosophila melanog
39	160	48.2	1507	24	ABK30352	Human G-protein-co
40	160	48.2	2642	24	ABT08500	Human novel protei
41	160	48.2	2649	24	AA597181	Human metallopept
42	160	48.2	2705	24	ABT08499	Human novel protei
43	160	48.2	2762	24	ABT08498	Human novel protei
44	160	48.2	3015	23	AA571731	DNA encoding novel
45	160	48.2	3431	22	AA055513	First splice varia

ALIGNMENTS

RESULT 1
AAD21439
ID AAD21439 standard; DNA, 1668 BP.
XX
AC AAD21439;
XX
DT 28-JAN-2002 (first entry)
XX
DE ADAM-23dis-Fc fusion construct DNA.
XX
DE Human; ADAM disintegrin domain; integrin; endothelial cell migration;
XX angiogenesis; ocular disorder; inflammatory disease; bone resorption;
XX osteoporosis; retinosis; thrombosis; tissue repair; wound healing;
XX retnopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
XX retrolental fibroplasia; inflammatory bowel disease; rubeosis; uveitis;
XX arthritis; rheumatism; myocardial infarction; coronary artery disease;
XX tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;

XX	Chimeric - Homo sapiens.
OS	Chimeric - Unidentified.
XX	
XX	
KW	ds.
KM	preclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;
KM	IgG, Fc region; antiinflammatory; osteopathic; vasotropic; chromolytic;
FT	Key
FT	CDS
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FT	/note= "IgK leader sequence"
FT	85..1644
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FT	93..954
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XX	
PN	WO200162905-A2.
PD	
XX	30-AUG-2001.
XX	
PF	23-FEB-2001; 2001WO-US05701.
XX	
PR	25-FEB-2000; 2000US-184865P.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Fanslow WC, Cerretti DP, Poindexter KM, Black RA;
XX	
DR	WPI: 2001-625725/72.
XX	
DR	P-PSDB: AAEI3055.
XX	
PT	Antagonizing the binding of an integrin to its ligand useful for the
PT	treatment of angiogenesis comprises administration of an
PT	ADAM-disintegrin domain polypeptide -
XX	
PS	Claim 14; Page 58-60; 66pp; English.
XX	
CC	The invention relates to the method and use of ADAM disintegrin domain
CC	polypeptides for inhibiting the biological activity of integrins,
CC	endothelial cell migration and angiogenesis. ADAM disintegrin domain
CC	polypeptides are used for treatment of ocular disorders, malignant and
CC	metastatic conditions, inflammatory diseases, osteoporosis and other
CC	conditions mediated by accelerated bone resorption, restenosis,
CC	inappropriate platelet activation, recruitment or aggregation, thrombosis
CC	or a condition requiring aggregation, thrombosis or a condition requiring
CC	tissue repair or wound healing, angiogenesis, ocular neovascularisation
CC	or solid tumour, diabetic retinopathy, retinopathy or prematurity,
CC	neovascular glaucoma, retinoblastoma, retrolental fibroplasia, rubeosis,
CC	uveitis, macular degeneration and corneal graft neovascularisation,
CC	inflammatory diseases, ocular tumours, diseases associated with chorioidal
CC	or iris neovascularisation, arthritis, rheumatism, inflammatory bowel
CC	disease, psoriasis, coronary artery disease or injury, myocardial
CC	infarction or injury following myocardial infarction, stroke, unstable
CC	angina, atherosclerosis, arteriosclerosis, preeclampsia, embolism,
CC	platelet-associated ischemic disorders including lung ischaemia,
CC	coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
CC	coronary intervention including angioplasty, atherectomy, stent placement
CC	and bypass surgery, thrombotic disorders including coronary artery
CC	thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC	peripheral artery thrombosis, venous thrombosis, thrombosis and
CC	coagulopathies associated with exposure to a foreign or injured tissue
CC	surface and recocclusion following thrombosis, deep venous thrombosis,
CC	pulmonary embolism, transient ischemic attacks and another conditions
CC	where vascular occlusion is a common underlying feature, in individuals
CC	at high risk for thrombus formation of reformation, advanced coronary

CC	artery disease, or for occlusion reocclusion, stenosis and/or restenosis
CC	of blood vessels or stroke benign tumours and preneoplastic conditions,
CC	myocardial angiogenesis, haemophilic joints, scleroderma, vascular
CC	adhesions, asthma and allergy, eczema and dermatitis, graft versus host
CC	disease, sepsis, adult respiratory distress syndrome, telangiectasia and
CC	wound granulation. The method are used in combination with angioplasty
CC	procedures, such as balloon angioplasty, laser angioplasty, coronary
CC	atherectomy or similar techniques, carotid endarterectomy, anastomosis of
CC	vascular grafts, surgery having a high risk of thrombus formation (1.e.
CC	coronary bypass surgery, insertion of a prosthetic valve or vessel and
CC	the like), atherectomy, stent placement, placement of a chronic
CC	cardiovascular device such as an in-dwelling catheter or prosthetic valve
CC	or vessel, organ transplantation or bypass surgery. The present sequence
CC	is a DNA encoding ADAM disintegrin domain polypeptide fusion construct.
CC	The fusion construct comprises of immunoglobulin K (IgK) leader, human
CC	ADAM disintegrin and Fc region.
XX	
XX	Sequence 1668 BP; 423 A; 444 C; 455 G; 346 T; 0 other;
SO	
Alignment Scores:	
Pred. No.:	2, 71e-30
Score:	332.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	100.00%
DB:	22
	Gaps: 0
US-09-634-252A-4_COPY 532_586 (1-55) x AAD21439 (1-1668)	
Oy	1 CysSerLeuSerAsnGlyValaHisCysSerAspGlyProCysCysAsnAnThrSerCys 20
Db	172 TGTTCCTCTCCACGCGGCTACTGTCAGCGACGCGGCCCTCTTAACATACCTATGT 231
Oy	21 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValaGlnGlyCysAspIleThrGln 40
Db	232 CTTTTCACGACGAGGGATGAATGCCGGATGCTGTGAACGAGTGTGATTACTGAA 291
Oy	41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
Db	292 TATTGTACTGGAGACTCTGTGTCAGTCCGCCACCAATCTTCAATAG 336
RESULT 2	
AA245826	standard; DNA; 2268 BP.
XX	
AC	AA245826;
XX	
DT	25-APR-2000 (first entry)
XX	
DE	DNA encoding a disintegrin homologue designated zdint1.
XX	
KW	Human; disintegrin homologue; zdint1; cardiac myocyte; adipocyte;
KW	gene therapy; cell-cell interaction; chondro sacroma; atherosclerosis;
KW	Alzheimer's disease; restenosis; ischemic reperfusion; obesity;
KW	intimal hyperplasia; tumour; platelet aggregation; apoptosis;
KW	neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
KW	connective tissue disorder; chondrogenesis; tumour proliferation;
KW	inflammation; ss.
OS	
XX	Homo sapiens.
XX	
EH	Location/Qualifiers
FT	3...2093
FT	/*tag= a
FT	/product= "zdint1"
XX	
PN	W0200002912-A2.
XX	
PD	20-JAN-2000.
XX	
XX	09-JUL-1999; 99WO-US15638.
XX	
PR	10-JUL-1998; 98US-0113883.

XX (ZYMO) ZYMOGENETICS INC.
PA Shepard PO, Baindur N, Deisher TA, Bishop PD;
XX WPI: 2000-160898/14.
XX P-PSDB: AA154457.
XX
XX Polypeptide useful in modulating cell-cell interaction in tissues of
PT heart, brain, spinal cord and treating chondro sarcoma,
PT atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -
XX
PS Example 1; Page 123-127; 132pp; English.
XX
CC The present sequence encodes a human disintegrin homologue, designated
CC zdn1. The zdn1 polypeptide is a cardiac myocyte proliferation and
CC differentiation stimulator, as well as an adipocyte proliferation and
CC differentiation inhibitor. Polynucleotides encoding zdn1 are used in
CC gene therapy. The zdn1 polypeptide is useful in modulating cell-cell
CC interactions of cells derived from tissues of heart, brain, spinal cord
CC and skeletal muscle. It is useful in treating and diagnosing chondro
CC sarcoma, atherosclerosis, Alzheimer's disease, restenosis, ischemic
CC reperfusion, obesity, intimal hyperplasia and tumors of heart, brain,
CC and spinal cord. The zdn1 polypeptide is also useful in identifying
CC its new family members, antagonists, agonists and antibodies.
CC Antagonists, antibodies and fusion proteins of zdn1 are useful in
CC inhibiting platelet aggregation, apoptosis, neurogenesis and myogenesis.
CC Agonists and antagonists are useful in studying cell-cell interactions,
CC arthritis, myogenesis, neurogenesis, connective tissue disorders,
CC chondrogenesis, tumour proliferation and suppression, extracellular
CC matrix proteins, repair and remodelling of ischemic reperfusion,
CC inflammation, and apoptosis.
XX
SQ Sequence 2268 BP; 654 A; 457 C; 558 G; 598 T; 1 other:
XX
Alignment Scores:
Pred. No.: 3.95e-30 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) x AA245826 (1-2268)
QY 1 CysSerLeuSerArgnGlyAlaHisCysSerAspGlyProCysCysAenAenThSerCys 20
Db 1227 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGCGGCTCTGTGAACAAATTAATCTCATGT 1286
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db 1287 CTTTTCAGCCACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1346
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
Db 1347 TATTGTACTGAGAGACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1391
RESULT 3
AA11991
ID AA11991 standard; cDNA: 2268 BP.
XX
AC AA11991;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human cDNA encoding partial disintegrin protease zdn1.
XX
XX Human; disintegrin; zdn1; ss; antiangiogenic; vascular; thrombolytic.
KW cell matrix; cell-cell interactions; apoptosis; neurogenesis;
KW connective tissue disorders; chondrogenesis; arthritis;
KW tumour proliferation; ischaemia reperfusion; inflammation;
KW chromosome 2q33.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
XX 3..2093
FT CDS
FT /**tag= a
FT /product= "zdn1"
FT /partial
FT /note= "No start codon"
FT 3..491
FT sig_peptide
FT /**tag= b
FT /note= "Encodes propeptide sequence"
FT 492..2090
FT mat_peptide
FT /**tag= c
FT /label= Mature_zdn1
XX
XX US6265199-B1.
XX
XX 24-JUL-2001.
XX
XX 09-JUL-1999; 99US-0351414.
XX
XX 10-JUL-1998; 98US-0092371.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Shepard PO, Baindur N, Deisher TA, Bishop PD, Taft DW;
XX WPI: 2001-450736/48.
XX P-PSDB: AAU07190.
XX
XX Disintegrins protease zdn1, useful for producing agents for the
XX development of antithrombotic and anti-migration of tumour cells and
XX have antiangiogenic activity -
XX
XX Example 1; Column 47-53; 50pp; English.
XX
XX The invention relates to an isolated novel disintegrin protease family
XX member, zdn1. Disintegrins bind cell surface molecules, including
XX integrins, on the surface of various cells such as platelets,
XX fibroblasts, tumour, endothelial, muscle, neuronal, bone and sperm cells.
XX Disintegrins are unique and potentially useful tools for investigating
XX cell matrix and cell-cell interactions, apoptosis, neurogenesis,
XX connective tissue disorders, chondrogenesis, arthritis, tumour
XX proliferation, ischaemia reperfusion and inflammation. Additionally, they
XX are useful in the development of antithrombotic and anti-migration of
XX tumour cells and have antiangiogenic activity. The present sequence
XX encodes human disintegrin, zdn1, the gene for which is located on
XX chromosome 2q33.
XX
SQ Sequence 2268 BP; 654 A; 457 C; 558 G; 598 T; 1 other;
XX
Alignment Scores:
Pred. No.: 3.95e-30 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) x AA11991 (1-2268)
QY 1 CysSerLeuSerArgnGlyAlaHisCysSerAspGlyProCysCysAenAenThSerCys 20
Db 1227 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGCGGCTCTGTGAACAAATTAATCTCATGT 1286
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db 1287 CTTTTCAGCCACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1346
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
Db 1347 TATTGTACTGAGAGACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1391

RESULT 4
ABO78447
ID ABO78447 standard; cDNA; 2268 BP.
XX
XX ABO78447;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Nucleotide sequence of human zdin1.
XX
XX Human; zdin1; disintegrin protease; platelet accumulation;
XX chromosome 2q33; platelet aggregation; proteolysis; apoptosis;
XX neurogenesis; myogenesis; connective tissue disorder; arthritis;
XX chondrogenesis; cell adhesion; neuron; myocyte; heart;
XX brain; spinal cord; skeletal muscle tissue; Alzheimer's disease;
XX tumor formation; multiple sclerosis; congestive heart failure;
XX ischaemic reperfusion; intimal hyperplasia; restenosis; gene; ss.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 3..2093
FT /tag= a
FT /product= "zdin1"
FT
FT
FT
XX US2002072102-A1.
XX
XX 13-JUN-2002.
XX
XX 16-MAR-2001; 2001US-0809790.
XX
XX 10-JUL-1998; 98US-092371P.
XX 09-JUL-1999; 99US-0351414.
XX
XX (SHEP/) SHEPPARD P O.
XX (BAIN/) BAINBUR N.
XX (DEIS/) DEISHER T A.
XX (BISH/) BISHOP P D.
XX
XX Shepard PO, Baindur N, Deisher TA, Bishop PD;
XX
XX WPI; 2002-598452/64.
XX P-PSDB; ABB78130.
XX
XX New disintegrin homolog polypeptide and polynucleotide, useful for
XX modulating cell-cell interactions and diagnosis; treatment of
XX Alzheimer's disease, tumor formation, multiple sclerosis and congestive
XX heart failure
XX
XX Claim 14; Page 26-29; 53pp; English.
XX
XX The present sequence encodes a human polypeptide designated zdin1.
XX zdin1 is a member of the disintegrin protease family. Zdin1 inhibits
XX platelet accumulation. The zdin1 gene is present on chromosome 2q33.
XX zdin1 polypeptides and polynucleotides are useful in treatment of
XX disorders associated with infarct in brain or heart tissue and/or
XX platelet aggregation, to modulate proteolysis, apoptosis, neurogenesis,
XX myogenesis, connective tissue disorders, arthritis, chondrogenesis,
XX cell adhesion, cell fusion, and signalling or to treat or prevent
XX development of pathological conditions in such diverse tissue as heart,
XX brain, spinal cord and skeletal muscle. The molecules modulate
XX inhibition and proliferation of neurons and myocytes in heart, brain,
XX spinal cord and skeletal muscle tissue. Disorders which may be amenable
XX to diagnosis, treatment or prevention with zdin1 polypeptides include,
XX Alzheimer's disease, tumor formation, multiple sclerosis, congestive
XX heart failure, ischaemic reperfusion or infarct and degenerative
XX diseases. The zdin1 molecules particularly useful in the treatment of
XX intimal hyperplasia or restenosis due to acute vascular injury.
XX
XX Sequence 2268 BP; 654 A; 457 C; 558 G; 598 T; 1 other;
XX
XX Alignment Scores:
XX Pred. No.: 3..95e-30 Length: 2268

Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) x ABO78447 (1-2268)
QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
DB 1227 TGTTCCTCTCCACGCGGCTCAGCGACGAGGCTCTGTAACAATACCTCATGT 1286
QY 21 LeupheginProArgGlyTyrGluCysArgAspAlaValaAsnGluCysAspIleThrGlu 40
DB 1287 CTTTTCAGCCACGAGGATGAAATGCCGGATGCTGTGAACGAGTGTATATTACTGAA 1346
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIle 55
DB 1347 TATTGTACTGAGGACTGTGTGATGATGCCACCAATCTTCAATAG 1391
RESULT 5
AAZ10207
ID AAZ10207 standard; DNA; 2499 BP.
XX
XX AAZ10207;
XX
XX 29-OCT-1999 (first entry)
XX
XX CDNA encoding the human SVP3-17 protein.
XX
XX SVP3-17; metalloproteinase-disintegrin; human chromosome 2;
XX human chromosome 7; malignant hyperthermia susceptibility;
XX Zellweger syndrome; neonatal adrenoleukodystrophy;
XX infantile Refsum disease; progressive familial intrahepatic cholestasis;
XX mucopolysaccharidosis VII; split hand/foot malformation;
XX arylsulphatase B deficiency; ventricular dysplasia-4; Coppock-like cataract;
XX insulin dependent diabetes mellitus-12; lamellar type ichthyosis;
XX transient neonatal myasthenia gravis; congenital aculeiform cataract;
XX juvenile amyotrophic lateral sclerosis;
XX familial paroxysmal choreoathetosis;
XX Finnish lethal neonatal metabolic syndrome; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT CDS 1..2499
XX FT /tag= a
XX
XX WO9941388-A2.
XX
XX 19-AUG-1999.
XX
XX 11-FEB-1999; 99WO-US03016.
XX
XX 11-FEB-1999; 98US-0074310.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Cerretti DP;
XX
XX WPI; 1999-527371/44.
XX P-PSDB; AAY30207.
XX
XX DNA encoding the SVP3-13 and SVP3-17 proteins for detecting
XX disease corresponding to chromosome 7, e.g. Zellweger syndrome
XX
XX Claim 1; Page 7-8; 82pp; English.
XX
XX The present sequence encodes a protein designated SVP3-17, which
XX is a member of the metalloproteinase-disintegrin family. The
XX specification also describes SVP3-13 proteins. Both sequences can
XX be used to identify human chromosome 2 or 7, and to map genes on these
XX two chromosomes, and also to identify genes associated with certain

CC diseases, syndromes, or other human conditions associated with human
CC chromosome 2 or 7. The disease that correspond to chromosome 7 include
CC malignant hyperthermia susceptibility, Zellweger syndrome, neonatal
CC adrenoleukodystrophy, infantile Refsum disease, progressive familial
CC intrapapillary colobomata, mucopolysaccharidosis VII, and split
CC hand/foot malformation. Diseases associated with chromosome 2 include
CC arrhythmogenic right ventricular dysplasia-4, insulin dependent diabetes
CC mellitus-12, transient neonatal myasthenia gravis, juvenile amyotrophic
CC lateral sclerosis, congenital aortic valve stenosis, Cypock-like cataract,
CC lamellar type ichthyosis, familial paroxysmal choreoathetosis, and
CC Finnish lethal neonatal metabolic syndrome.

XX SQ Sequence 2499 BP; 677 A; 593 C; 645 G; 584 T; 0 other;

Alignment Scores:

Pred. No.:	4,466-30	Length:	2499
Score:	332.00	Matches:	55
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-634-252a-4_COPY_532_586 (1-55) x AA210207 (1-2499)

OY 1 CysSerLeuSerAenGlyAlaHisCysSerAenGlyProCysCysAenAenThSerCys 20
DB 1594 TGTTCCTCTCCAAAGGGGCTCACTGCAGCGAGGGCCCTGTAACAATACCTCATGT 1653

OY 21 LeuPheGlnProAenGlyTyrGluCysAenAenAenAenAenGluCysAenAenThSerGlu 40
DB 1654 CTTTTCAGCCAGAGGATGAATGCCGGATGCTGTAACGAGTGTGATATTACTGAA 1713

OY 41 TyrCysThrGlyAenSerGlyGlnCysProProAenLeuHisLys 55
DB 1714 TATTGTACTGAGACTCTGTGATGAGTGTGTAACGAGTGTGATATTACTGAA 1758

RESULT 6

AAx78438 standard; cDNA to mRNA; 3054 BP.

XX AC AAX78438;

XX DT 26-AUG-1999 (first entry)

XX DE Human MDC3 cDNA.

XX KW Metalloproteinase-like-disintegrin-like cysteine rich protein; human;

XX KM MDC2-alpha; MDC2-beta; MDC3; medical; treatment; diagnosis; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 224..2722

XX FT /*tag= a

XX FT /product= "MDC3"

XX PN JP1155574-A.

XX PD 15-JUN-1999.

XX PF 01-DEC-1997; 97JP-0330020.

XX PR 01-DEC-1997; 97JP-0330020.

XX PA (EISA) EISAI CO LTD.

XX DR WPI; 1999-398071/34.

XX DR P-PSDB; AAY25120.

XX PT New protein belonging to MDC gene family - useful in medical

XX treatment and diagnosis

XX Claim 17; Page 13-16; 17pp; Japanese.

XX CC This invention describes novel human MDC2-alpha, MDC2-beta and MDC3
XX CC proteins and their encoding nucleic acids. The products of the invention
XX CC are useful in medical treatment and diagnosis.

XX SQ Sequence 3054 BP; 815 A; 754 C; 803 G; 682 T; 0 other;

Alignment Scores:

Pred. No.:	5,76-30	Length:	3054
Score:	332.00	Matches:	55
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-634-252a-4_COPY_532_586 (1-55) x AAX78438 (1-3054)

OY 1 CysSerLeuSerAenGlyAlaHisCysSerAenGlyProCysCysAenAenThSerCys 20
DB 1817 TGTTCCTCTCCAAAGGGGCTCACTGCAGCGAGGGCCCTGTAACAATACCTCATGT 1876

OY 21 LeuPheGlnProAenGlyTyrGluCysAenAenAenAenAenGluCysAenAenThSerGlu 40
DB 1877 CTTTTCAGCCAGAGGATGAATGCCGGATGCTGTAACGAGTGTGATATTACTGAA 1936

OY 41 TyrCysThrGlyAenSerGlyGlnCysProProAenLeuHisLys 55
DB 1937 TATTGTACTGAGACTCTGTGATGAGTGTGTAACGAGTGTGATATTACTGAA 1981

RESULT 7

ABx76201 standard; DNA; 3054 BP.

XX AC ABX76201;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polynucleotide #72.

XX KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;

XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PE 18-APR-2002; 2002WO-US12476.

XX PR 18-APR-2001; 2001US-284770P.

XX PR 10-MAY-2001; 2001US-290492P.

XX PR 09-NOV-2001; 2001US-339245P.

XX PR 13-NOV-2001; 2001US-350665P.

XX PR 29-NOV-2001; 2001US-334370P.

XX PR 12-APR-2002; 2002US-372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX DR P-PSDB; ABUS6479.

XX PT Detecting a lung cancer-associated transcript in a cell from a patient

XX PT for treating lung cancer, by contacting a biological sample from the

XX PT patient with a polynucleotide that exhibits increased or decreased

XX PT expression in lung cancer

XX Claim 22; Page 243; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
CC polynucleotides of the invention.

XX Sequence 3054 BP; 815 A; 754 C; 803 G; 682 T; 0 other;

Alignment Scores:
Pred. No.: 5, 7e-30 Length: 3054
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x ABX76201 (1-3054)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysGlyAsnAsnThrSerCys 20
1817 TGTTCCTCTCCAAAGGGGCTCACTGACGAGCGGGCCCTGCTGTAACAAATCCTCATGT 1876

QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
1877 CTTTTCACGCCAGAGGATGATGATCCGGGATGCTGTACAGAGTGATATTACTGAA 1936

QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
1937 TATTGACTGGAGACTCTGTCAGTCCACCAAAATCTTCATMAG 1981

RESULT 8

ABX76292
ID ABX76292 standard; DNA; 3054 BP.

XX ABX76292;
XX 02-APR-2003 (first entry)

XX Lung cancer-associated polynucleotide #156.
XX Lung cancer-associated polynucleotide; gene; ds; cytosolic; emphysema;
XX antiinflammatory; antiasbestatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.
XX MO200286443-A2.

XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.
XX 10-MAY-2001; 2001US-280492P.
XX 09-NOV-2001; 2001US-339245P.
XX 13-NOV-2001; 2001US-350666P.

PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI; 2003-093161/08.
XX P-PSDB; ABUS6563.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer
XX
XX Claim 22; Page 307-308; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
CC polynucleotides of the invention.

XX Sequence 3054 BP; 815 A; 754 C; 803 G; 682 T; 0 other;

Alignment Scores:
Pred. No.: 5, 7e-30 Length: 3054
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x ABX76292 (1-3054)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysGlyAsnAsnThrSerCys 20
1817 TGTTCCTCTCCAAAGGGGCTCACTGACGAGCGGGCCCTGCTGTAACAAATCCTCATGT 1876

QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
1877 CTTTTCACGCCAGAGGATGATGATCCGGGATGCTGTACAGAGTGATATTACTGAA 1936

QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
1937 TATTGACTGGAGACTCTGTCAGTCCACCAAAATCTTCATMAG 1981

RESULT 9

AAI72025
ID AAI72025 standard; cDNA; 4043 BP.

XX AAI72025;
XX 04-MAR-2002 (first entry)

XX ADAM 23 cDNA.
XX Disintegrin; ADAM 23; metalloproteinase; domain; adhesion; proteolysis;
XX modulator; alpha-v-beta3 integrin; tumour progression; neural tissue;

KW angiogenesis; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 1017..3515
FT /tag= a
FT /product= "ADAM 23"
XX
XX MO200174857-A2.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001; 2001WO-US10729.
XX
XX 03-APR-2000; 2000US-194164P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Lopez-Ortin C, Freiji JMP, Bianchi AB, Miguel SC, Garcia JML;
XX Trail P;
XX
XX WPI; 2002-066298/09.
XX P-PSDB; AAB47778.
XX
XX Nucleic acid encoding a new ADAM family member, designated ADAM 23 is
XX useful to find modulators of its interaction with integrin which can be
XX used to prevent angiogenesis or increase neural growth.
XX
XX Claim 2, Page 36-38, 44pp; English.
XX
XX This sequence encodes a cellular disintegrin, ADAM 23, which is a
XX protein having a disintegrin and metalloproteinase domain. This
XX protein can perform both adhesion and proteolysis functions. This
XX Modulators of the interaction between ADAM and alpha-v-beta3 integrin
XX are used to inhibit tumour progression or induce growth of neural
XX tissue. These compounds modulate angiogenesis and induction of matrix
XX metalloproteinases facilitating migration of tumour cells and growth of
XX neural tissue.
XX
XX Sequence 4043 BP; 1110 A; 946 C; 1002 G; 985 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 8.06e-30 Length: 4043
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) x AA172025 (1-4043)
QY 1 CysSerLeuSerAenGlyAlaHisCysSerAspGlyProCysCysAenAenThrSerCys 20
DB 2610 TGTTCCTCTCCAAACGGGGCTCACTGCAGCAGCGGGCTGTAACTACTCTCATGT 2669
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
DB 2670 CTTTTCAGCCACGAGGATGAATGCCGGGATCTGTGAACGAGTGTGATATTACGAA 2729
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
DB 2730 TATTGTACTGGAGACTCTGTCAGTCCGCCCAATATCTTCAATAG 2774
RESULT 10
AA245827
ID AA245827 standard; DNA; 2088 BP.
XX
XX AA245827;
XX
XX 25-APR-2000 (first entry)
DT
DE Degenerate DNA encoding a disintegrin homologue designated zdint1.

XX
XX Human; disintegrin homologue; zdint1; cardiac myocyte; adipocyte;
XX gene therapy; cell-cell interaction; chondro sarcoma; atherosclerosis;
XX Alzheimer's disease; restenosis; ischemic reperfusion; obesity;
XX intimal hyperplasia; tumour; platelet aggregation; apoptosis;
XX neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
XX connective tissue disorder; chondrogenesis; tumour proliferation;
XX inflammation; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO200002912-A2.
XX
XX 20-JAN-2000.
XX
XX
XX 09-JUL-1999; 99WO-US15638.
XX
XX 10-JUL-1998; 98US-0113883.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Bairdur N, Deisher TA, Bishop PD;
XX
XX WPI; 2000-160898/14.
XX
XX Polypeptide useful in modulating cell-cell interaction in tissues of
XX heart, brain, spinal cord and treating chondro sarcoma,
XX atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -
XX
XX Disclosure; Page 129-130; 132pp; English.
XX
XX The present sequence represents a degenerate sequence which encodes
XX a human disintegrin homologue, designated zdint1. The zdint1 polypeptide
XX is a cardiac myocyte proliferation and differentiation stimulator, as
XX well as an adipocyte proliferation and differentiation inhibitor.
XX Polynucleotides encoding zdint1 are used in gene therapy. The zdint1
XX polypeptide is useful in modulating cell-cell interactions of cells
XX derived from tissues of heart, brain, spinal cord and skeletal muscle.
XX It is useful in treating and diagnosing chondro sarcoma, atherosclerosis,
XX Alzheimer's disease, restenosis, ischemic reperfusion, obesity, intimal
XX hyperplasia and tumors of heart, brain, and spinal cord. The zdint1
XX polypeptide is also useful in identifying its new family members,
XX antagonists, agonists and antibodies. Antagonists, antibodies and fusion
XX proteins of zdint1 are useful in inhibiting platelet aggregation,
XX apoptosis, neurogenesis and myogenesis. Agonists and antagonists are
XX useful in studying cell-cell interactions, arthritis, myogenesis,
XX neurogenesis, connective tissue disorders, chondrogenesis, tumour
XX proliferation and suppression, extracellular matrix proteins, repair
XX and remodelling of ischemic reperfusion, inflammation, and apoptosis.
XX
XX Sequence 2088 BP; 412 A; 178 C; 381 G; 262 T; 855 other;
SQ
Alignment Scores:
Pred. No.: 1.63e-24 Length: 2088
Score: 285.00 Matches: 45
Percent Similarity: 81.82% Conservative: 0
Best Local Similarity: 81.82% Mismatches: 10
Query Match: 85.84% Indels: 0
DB: 21 Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) x AA245827 (1-2088)
QY 1 CysSerLeuSerAenGlyAlaHisCysSerAspGlyProCysCysAenAenThrSerCys 20
DB 1225 TGYWMSNYTMSNAAYGNGCNCAYTGYWMSNGAAGCNCNGYGYAAVAAVACNWSNTGY 1284
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
DB 1285 YTTTTCARCCNNGNGNTYGAATGYMGNGAIGCNGTNAAYGARFGYGAATACNGAR 1344
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

Mon Oct 27 15:28:03 2003

us-09-634-252a-4_copy_532_586.p2n.rng

Page 8

Db 1345 TAYTYACNGNGAYWSNGNCARTGYCCNCAAYTNCAYAR 1389

Search completed: October 21, 2003, 10:34:17
Job time : 148.862 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:21:31 ; Search time 1304.78 Seconds
(without alignments)
1024.499 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586
Perfect score: 332
Sequence: 1 CSLSNGAHCSDGPCNNNTSC.....CDITEYCTGDSGQCPNLMHK 55

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45362784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgrp2.1/USPTO.spool/US09634252/runat.21102003.090324.3331/app.query.fasta.1.462
-DB=EST -QFMT=fa+cap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human10.cdi -LIST=45
-DOCLALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=10 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09634252 @CGN 1.1 3596 @runat.21102003.090324.3331 -NCPU=6 -ICPU=3
-NO.MMAP -LARGESUBSTR -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: EST:*
2: em_estba:*
3: em_esthum:*
4: em_estlin:*
5: em_estmu:*
6: em_estov:*
7: em_estpl:*
8: em_estro:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_ylt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	100.0	553	10	AW961362 ESTJ73434
2	332	100.0	728	13	BUS39967 AGENCOURT
3	332	100.0	752	10	BF691008 602247043
4	328	98.8	340	14	F08148 HSC2RF011.n
5	320	96.4	722	12	BI184544 UNL-P-FN-
6	319	96.1	470	14	CB733332 AMGNNUC:N
7	319	96.1	2891	11	AK046677 Mus muscu
8	319	96.1	3433	11	AK029301 Mus muscu
9	319	96.1	3498	11	AK034022 Mus muscu
10	318	95.8	432	12	BI018895 IL3-MT026
11	308	92.8	261	9	AA317222 ESTJ19173
12	305	91.9	652	9	AV340595 AV340595
13	299	90.1	402	12	BI019679 BI019679
14	293	88.3	326	14	RI15038 RI15038
15	286.5	86.3	648	13	BUS396219 BUS396219
16	286.5	86.3	660	13	BUS395688 603805442
17	286.5	86.3	661	13	BUS395688 603805095
18	271.5	81.8	579	12	BI844587 603804456
19	271.5	81.8	583	12	BI844587 603804456
20	269	81.0	405	14	R52569 R52569
21	268	80.7	428	9	AA718688 AA718688
22	266.5	80.3	664	12	BI429326 BI429326
23	264.5	79.7	598	12	BI981504 BI981504
24	264.5	79.7	616	12	BI476560 BI476560
25	264.5	79.7	652	12	BI429301 BI429301
26	262.5	79.1	648	13	BUS31413 BUS31413
27	260.5	78.5	599	12	BM070858 BM070858
28	259	78.0	447	10	BF905823 IL3-MT026
29	226.5	68.2	512	12	BI839501 BI839501
30	213	64.2	443	14	CB788730 CB788730
31	213	64.2	513	14	CB716849 CB716849
32	213	64.2	609	14	CB580769 CB580769
33	213	64.2	704	14	BY722939 BY722939
34	212	63.9	471	14	CB732873 CB732873
35	210	63.3	526	12	BI839959 BI839959
36	207	62.3	570	13	BQ833435 BQ833435
37	201	60.5	481	13	BY255403 BY255403
38	190	57.2	375	9	AA511039 AA511039
39	185.5	55.9	397	10	AW898896 AW898896
40	185	55.7	690	12	BJ059956 BJ059956
41	184	55.4	618	12	BJ495352 BJ495352
42	176	53.0	622	14	CB578552 CB578552
43	171	51.5	400	14	CB523459 CB523459
44	170	51.2	583	12	BI032916 BI032916
45	168.5	50.8	334	9	AL047647 AL047647

ALIGNMENTS

RESULT 1
LOCUS AW961362 553 bp mRNA linear EST 01-JUN-2000
DEFINITION ESTJ73434 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AW961362
VERSION AW961362.1 GI:8151046
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 553)
Hegde,P., Qi,R., Aderthy,K., Dharep,S., Gaspard,R., Gay,C., Holt

TITLE
JOURNAL
COMMENT

I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: john@igir.org
Plate: 157
Seq primer: Reverse.
Location/Qualifiers
1..553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1ib="MAGE_resequences, MAGC"
/note="Vector: pBluescriptSKm"

BASE COUNT 149 a 113 c 148 g 143 t
ORIGIN

Alignment Scores:
Pred. No.: 9,48e-28 Length: 553
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x AW961362 (1-553)

QY 1 CysSerLeuSerArgGlyAlaHisCysSerArgGlyProCysCysAsnAsnThrSerCys 20
47 TGTTCCTCTCCACGCGGCTCTCATGCGACGCGGCTCTGTATCAATACCTCATGT 106
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
107 CTTTTCAGCCACGAGGGGTATGATGATGCGGGATGCTGTACGATGATTTCTGAA 166
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
167 TATTGTACTGGAGACTGTGTCAGTCCACCAAAATCTTCATTAAG 211
DB

RESULT 2 BUS39967 728 bp mRNA linear EST 13-SEP-2002
LOCUS BUS39967
DEFINITION AGENCOURT_10254064 NIH_MGC_128 Homo sapiens cDNA clone
IMAGE:6570971 5', mRNA sequence.
ACCESSION BUS39967
VERSION BUS39967.1 GI:22850408
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 728)
NIH-MGC http://mgc.mci.nih.gov/
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2760 row: 1 column: 11
High quality sequence stop: 527.
Location/Qualifiers

FEATURES

source

1..728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1ib="MAGE:6570971"
/issue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_1ib="NIH_MGC_128"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccatcctggc); Site 2: SfiI (ggccgcctggc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTGATCAACGAGGAGTGGCCATTAGCGCCGGG-3' and 5'-ATTCTAGAGCGGAGCGCGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_127). Library created in the laboratory of T. Uedini, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."

BASE COUNT 213 a 142 c 210 g 162 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.36e-27 Length: 728
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x BUS39967 (1-728)

QY 1 CysSerLeuSerArgGlyAlaHisCysSerArgGlyProCysCysAsnAsnThrSerCys 20
365 TGTTCCTCTCCACGCGGCTCTCATGCGACGCGGCTCTGTATCAATACCTCATGT 424
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
425 CTTTTCAGCCACGAGGGGTATGATGATGCGGGATGCTGTACGATGATTTCTGAA 484
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
485 TATTGTACTGGAGACTGTGTCAGTCCACCAAAATCTTCATTAAG 529
DB

RESULT 3 BF691008 752 bp mRNA linear EST 22-DEC-2000
LOCUS BF691008
DEFINITION 602247043F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332275 5',
mRNA sequence.
ACCESSION BF691008
VERSION BF691008.1 GI:11976416
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 752)
NIH-MGC http://mgc.mci.nih.gov/
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.mci.nih.gov/
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

Found through the I.M.A.G.E. Consortium/LML at:
http://image.llnl.gov
Plate: L10M198 row: e column: 12
High quality sequence stop: 719.
Location/Qualifiers

FEATURES

source

1..752

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4332275"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NH MGC_62"
/note="Organ: skin; Vector: pDR-LIB (Clontech); Site_1:
SfiI (ggcgccctggcc); Site_2: SfiI (ggccatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTATGCG-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 195 a 151 c 217 g 189 t
ORIGIN

Alignment Scores:

Pred. No.: 1,42e-27 Length: 752
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x BF691008 (1-752)

Oy 1 CysSerLeuSerAenGlyAlaHisCysSerAenGlyProCysAsnAsnThrSerCys 20
Db 73 TGTTCCTCTCCACAGGGGCTCAGCGACGAGGGCCCTGCTTAACAATCTCATGT 132
Oy 21 LeupheginProAenGlyTYrGluCysArgAspAlaValaAsnGluCysAspIleThrGlu 40
Db 133 CTTTTCAGCCACGAGGATGAATGCCGGATGCTGTGAACGAGTGATATTACTGAA 192
Oy 41 TYrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
Db 193 TATTGTACTGGAGACTCTGTCAGTCCACCAATCTTCAATAG 237

RESULT 4

F08148 340 bp mRNA linear EST 21-FEB-1995

LOCUS HSCRF01 normalized infant brain cDNA Homo sapiens cDNA clone
c-2rf01, mRNA sequence.

ACCESSION

F08148 F08148.1 GI:677656

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

Auffray, C., Behar, G., Bois, F., Bouchier, C., de Silva, C., Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Jamy, B., Lorenzo, F., Sebastiani-Kabakchis, C. and Tessier, A.

TITLE

IMAGE: molecular integration of the analysis of the human genome and its expression

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

CONTACT: Genethon

Genexpress-Genethon

Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress library_id: C; Genexpress_sequence_id: y1c-2rf01
Seq primer: (-21)M3 universal.
Location/Qualifiers

FEATURES

source

1..340

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-2rf01"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: latmid BA; Site_1: HindIII;
Site_2: NotI; sex:Female; dev stage=3 months old;
isolate=muscular atrophy patient; tissue type=total brain
; total mRNA was oligo-(dt) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
latmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization method:
Bento Soares, P.N.A.S. in press"

BASE COUNT 87 a 70 c 90 g 84 t 9 others
ORIGIN

Alignment Scores:

Pred. No.: 1,41e-27 Length: 340
Score: 328.00 Matches: 54
Percent Similarity: 98.18% Conservative: 0
Best Local Similarity: 98.18% Mismatches: 1
Query Match: 98.80% Indels: 0
DB: 14 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x F08148 (1-340)

Oy 1 CysSerLeuSerAenGlyAlaHisCysSerAenGlyProCysAsnAsnThrSerCys 20
Db 132 TGTTCCTCTCCACAGGGGCTCAGCGACGAGGGCCCTGCTTAACAATCTCATGT 191
Oy 21 LeupheginProAenGlyTYrGluCysArgAspAlaValaAsnGluCysAspIleThrGlu 40
Db 192 CTTTTCAGCCACGAGGATGAATGCCGGATGCTGTGAACGAGTGATATTACTGAA 251
Oy 41 TYrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
Db 252 TATTGTACTGGAGACTCTGTCAGTCCACCAATCTTCAATAG 296

RESULT 5

B1184544/c 722 bp mRNA linear EST 10-JUL-2001

LOCUS UNL-P-FN-co-e-05-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-co-e-05-0-UNL.3', mRNA sequence.

ACCESSION

B1184544 B1184544.1 GI:14658953

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

TITLE

Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles

JOURNAL Mamm. Genome 14 (1), 65-70 (2003)

CONTACT: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln

Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dcomp@unl.edu

The sequence contained an oligo-dt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The following repetitive elements were found in this cDNA sequence: 3-43, >(TAAA)n#simple_repeat
Seq primer: M13 -29
POLYA=yes

FEATURES

source

1..722
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-co-e-05-0-UNL"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pTR3D-Pac (Pharmacia) with a modified polylinker, Site_1: Not I; Site_2: Eco RI; The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dt track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996.

Alignment Scores:
Pred. No.: 3,06e-26 Length: 722
Score: 330.00 Matches: 53
Percent Similarity: 98.18% Conservative: 1
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 96.39% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x B1184544 (1-722)

BASE COUNT 188 a 181 c 131 g 222 t

ORIGIN

1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThreSerCys 20
640 TGCTCTCTCTCCACGCGTCCCGACGACGCGGCCCTGCTGTAATGATGATCTCATGT 581
21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
580 CTTTTCACGCCACGTCGGGATGATGATGTCGGGATGCTGTAATGATGATGATTTACCGAA 521

41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
520 TATTGACTGAGAGACTCTGCCACGTCGCCCAAAATCTTCATAG 476

RESULT 6

LOCUS

CB733332 470 bp mRNA linear EST 11-APR-2003

DEFINITION

AMGNNUC:NRHY5-00422-H8-A W Rat hypothalamus (10471) Rattus norvegicus cDNA clone nrhy5-00422-h8 5', mRNA sequence.

ACCESSION

CB733332.1 GI:29800497

VERSION

CB733332.1

KEYWORDS

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 470)

AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00422 row: h column: 8.

FEATURES

source

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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy5-00422-h8"
/note="Vector: pSPORFL, Site_1: SalI; Site_2: NotI; W Rat hypothalamus adult female wistar rat avg. insert size 2.3 kb fraction 6 and 7"

BASE COUNT 124 a 111 c 137 g 98 t

ORIGIN

Alignment Scores:
Pred. No.: 2,25e-26 Length: 470
Score: 319.00 Matches: 53
Percent Similarity: 96.36% Conservative: 0
Best Local Similarity: 96.36% Mismatches: 2
Query Match: 96.08% Indels: 0
DB: 14 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x CB733332 (1-470)

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165 TGCTCTCTCTCCACGCGGCGCCACGTCGACGACGCGGCCCTGCTGTAATGATGATCTCATGT 224
21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
225 CTTTTCACGTCACGAGGTGATGATGTCGGGATGCTGTAATGATGATGATTTACCGAA 284
41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
285 TACTGCACCGAGACTCTGCCACGTCGCCCGCGAATCTGCATAAA 329

RESULT 7

LOCUS

AK046677 2891 bp mRNA linear HTC 05-DEC-2002

DEFINITION

Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B43037120 Product:a disintegrin and metalloprotease domain 23, full insert sequence.

ACCESSION

AK046677.1 GI:26091652

VERSION

AK046677.1

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Carninci, P. and Hayashizaki, Y.

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Maitahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
Genome Res. 10 (11), 1757-1771 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20530913
11076861

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Akakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Katsukawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staahl, F., Suzuki, F., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojling, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gestblom, S., Hill, D., Hofmann, M., Hume, D.A., Kamihara, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Konturki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

21085660
11217851

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2891)
Adachi, J., Aizawa, K., Akiyama, T., Akakawa, T., Eono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirokane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

TITLE
JOURNAL

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
SOURCE

1..2891
location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"

/strain="C57BL/6J"
/db_xref="FANTOM:DB:B430307120"
/db_xref="taxon:10090"
/clone="B430307120"
/sex="male"
/tissue_type="adipose"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="4 days neonate"
1..2891
/note="a disintegrin and metalloprotease domain 23 (MCD|MG1:1345162, GB|NM_011780, evidence: BLASTN, 100%, match=2431)"

BASE COUNT
ORIGIN

721 a 794 c 778 g 598 t

Alignment Scores:
Score: 2.48e-25
Percent Similarity: 319.00
Best Local Similarity: 96.36%
Query Match: 96.08%
DB: 11 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x AK046677 (1-2891)

OY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1906 TGTTGGCTCTCCAAATGGGGCCCACTGAGTGCAGGGCCCTGCTGTAAACACACTCATGT 1965

OY 21 LeuPheGlnProArgGlyTyrGlyCysArgAspAlaValAsnGlyCysAspIleThrGlu 40
Db 1966 CTTTTCAGTCACGAGGAGTGAATGTCGGAGATGCCGTAACAGCTGTGATATCACCAG 2025

OY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 2026 TACTGCACGTGAGACTCTGGCCAGTCCACCGAACCCTCATATAA 2070

RESULT 8
AK029301
LOCUS
DEFINITION
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832416K07 product:a disintegrin and metalloprotease domain 23, full insert sequence.

ACCESSION
AK029301
VERSION
AK029301.1 GI:26081272
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636

REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Maitahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

misc_feature
1..3433
/note="a disintegrin and metalloprotease domain 23
(MGI|MGI:1345162, GBLNM_011780, evidence: BLASTN, 100%,
match=2431)"
BASE COUNT 944 a 792 c 836 g 861 t
ORIGIN

Alignment Scores:

Pred. No.:	3,11e-25	Length:	3433
Score:	319.00	Matches:	53
Percent Similarity:	96.36%	Conservative:	0
Best Local Similarity:	96.36%	Mismatches:	2
Query Match:	96.08%	Indels:	0
DB:	11	Gaps:	0

US-09-634-252a-4_COPY_532_586 (1-55) x AK029301 (1-3433)

Qy 1 CysSerLeuSerArgGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1207 TGTTCGCTCTCCATGGGGCCCACTGACGATGACGGCCCTGCTGAACACACCTCATGT 1266

Qy 21 LeuPheGlnProAaGlyGlyTyrGluCysArgAspAlaValaIaengluCysAspIleThrGlu 40
Db 1267 CTTTTCAGTCACGAGGATGATGAATGTCGGGATGCCGTAACACGCTGTGATATACCGAG 1326

Qy 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
Db 1327 TACTGCACTGGAGACTCTGGCCACTGCCACCACTCCATTA 1371

RESULT 9
AK034022
LOCUS
DEFINITION

AK034022 3498 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male diencephalon cDNA, RIKEN full-length
enriched library, clone:930142P22 product: a disintegrin and
metalloprotease domain 23, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK034022
AK034022.1 GI:26329622
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, U., Nishi, K., Kitanishi, T., Tashiro, H., Itoh, M.,
Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yanamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Matsubiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kawaga, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shikata, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-research-riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

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/clone="4832416K07"
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FEATURES
SOURCE

1..3433
/organism="Mus musculus"
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/db_xref="FANTOM DB:4832416K07"
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1..3433
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1..3433
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1..3433
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1..3433
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/clone="4832416K07"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"

Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Katsukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Resple, G., Suzuki, F., Tomita, M., Quackenbush, J., Schriml, L.M., Staub, J., Suzuki, F., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Bader, R., Barash, G., Blake, J., Boffelli, D., Bojunga, M., Aono, H., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauris, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontecki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

21085660
11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 3498)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Eono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Iehi, Y., Itoh, M., Kagawa, I., Katsukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T., Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-42 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-3222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedic Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/.
location/Qualifiers

1. 3498

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BASE COUNT 906 a 880 c 853 g 859 t

ORIGIN

Alignment Scores:
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Score: 319.00 Matches: 53
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DB: 11 Gaps: 0

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Db 1947 CTTTTCAGTCACGAGGATGATGTCGGGATGCCCTTAACACACTGTGATATCACCAG 2006

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RESULT 10
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LOCUS
DEFINITION H3-MT0267-050101-436-B07 MT0267 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI018895
VERSION BI018895.1 GI:14425525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 432)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W., Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663
10737800

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Genome

Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL3&e2=IL3-MT0267-
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 Seq primer: puc 18 forward
 High quality sequence stop: 429.
 Location/Qualifiers

FEATURES

Source

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1..432
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from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

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BASE COUNT 119 a 100 c 113 g 100 t
 ORIGIN

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DB:	12	Gaps:	0

US-09-634-252a-4_COPY_532_586 (1-55) x B101895 (1-432)

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			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	5	T	C	C	T	C	T	C	T	C	A	C	G	G	G	C	T	C	A	C	G	G	C	C	C	T	G	C	T	G	T	A	C	A	T	A	C	T	C	T	A	T	G	T	C	T	64											
OY	22	P	h	e	g	i	n	P	r	o	A	r	g	i	y	T	r	G	i	n	C	y	S	a	r	g	A	p	a	l	a	v	a	I	a	s	n	G	i	n	C	y	S	a	s	p	i	e	r	h	r	G	i	n	T	y	r	41
			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	65	T	T	T	C	A	C	C	A	C	G	G	C	G	T	A	T	G	A	T	G	C	C	G	G	A	T	G	C	T	G	T	G	A	A	C	G	A	G	A	T	T	A	C	T	A	C	T	G	A	T	A	T	124				
OY	42	C	y	S	t	h	r	G	i	n	A	s	p	S	e	r	G	i	n	C	y	S	e	r	P	r	o	A	e	n	L	e	u	H	i	s	I	s	55																			
			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
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Search completed: October 21, 2003, 13:06:58
 Job time : 1308.78 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:34:26 ; Search time 108.654 Seconds
(without alignments)
758.947 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTKLFEPTECGYVEAGEE.....CPPNLHKDQYACNQCRC 104

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1840717 seqs, 76133381 residues

Total number of hits satisfying chosen parameters: 3681434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-THR MIN=0 -ALIGN=10 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09634252@cgn_1.1.248 @runat_21102003_090326_3471
-NCPU=6 -ICPU=3 -NO_MMAP -LANG=QUEBERT -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Pending Patente NA New:*

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7: /cgn2_6/pdata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	630	100.0	3760	7	US-60-495-114-329
2	630	100.0	4071	7	US-60-495-114-330
3	404.5	64.2	1911	7	US-60-487-610-948
4	404.5	64.2	1911	7	US-60-485-450-577
5	404.5	64.2	3117	7	US-60-495-114-825
6	404.5	64.2	3167	7	US-60-487-610-947
7	404.5	64.2	3167	7	US-60-485-450-576
8	404.5	64.2	3185	7	US-60-487-610-949
9	404.5	64.2	3185	7	US-60-485-450-578
10	404.5	64.2	3421	7	US-60-495-114-827
11	404.5	64.2	3431	7	US-60-495-114-826

12	404.5	64.2	3433	7	US-60-495-114-828	Sequence 828, App
13	363.5	57.7	2636	7	US-60-490-890-1042	Sequence 1042, Ap
14	363.5	57.7	2744	7	US-60-490-890-1038	Sequence 1038, Ap
15	363.5	57.7	2775	7	US-60-495-114-168	Sequence 168, App
16	363.5	57.7	2775	7	US-60-495-114-173	Sequence 173, App
17	363.5	57.7	2865	7	US-60-495-114-174	Sequence 174, App
18	363.5	57.7	2876	7	US-60-495-114-166	Sequence 166, App
19	363.5	57.7	3347	7	US-60-490-890-1040	Sequence 1040, Ap
20	363.5	57.7	3759	7	US-60-495-114-172	Sequence 172, App
21	363.5	57.7	3777	7	US-60-495-114-169	Sequence 169, App
22	363.5	57.7	3777	7	US-60-495-114-175	Sequence 175, App
23	363.5	57.7	3801	7	US-60-495-114-171	Sequence 171, App
24	363.5	57.7	3819	7	US-60-495-114-167	Sequence 167, App
25	363.5	57.7	3819	7	US-60-495-114-170	Sequence 170, App
26	363.5	57.7	3867	7	US-60-495-114-176	Sequence 176, App
27	363.5	57.7	3878	7	US-60-495-114-165	Sequence 165, App
28	292	46.3	2523	1	PCT-US03-30720-591	Sequence 591, App
29	292	46.3	3271	6	US-10-670-184-1	Sequence 1, Appl1
30	292	46.3	3390	6	US-10-670-184-2	Sequence 2, Appl1
31	292	46.3	3445	7	US-60-495-114-964	Sequence 964, App
32	292	46.3	3482	7	PCT-US03-30720-267	Sequence 267, App
33	292	46.3	3523	7	US-60-495-114-965	Sequence 965, App
34	292	46.3	3554	1	PCT-US03-28227-1868	Sequence 1868, Ap
35	292	46.3	3582	6	US-10-670-184-3	Sequence 3, Appl1
36	292	46.3	3606	1	PCT-US03-28227-1890	Sequence 1890, Ap
37	292	46.3	3721	1	PCT-US03-28227-1889	Sequence 1889, Ap
38	278	44.1	2815	1	PCT-US03-28751-6	Sequence 6, Appl1
39	274	43.5	1194	1	PCT-US03-26780-217	Sequence 217, App
40	274	43.5	2286	7	US-60-495-114-447	Sequence 447, App
41	274	43.5	2313	7	US-60-495-114-448	Sequence 448, App
42	274	43.5	2336	7	US-60-495-114-449	Sequence 449, App
43	274	43.5	2712	7	US-60-487-610-511	Sequence 511, App
44	274	43.5	2740	1	PCT-US03-28751-3	Sequence 3, Appl1
45	274	43.5	2740	7	US-60-490-890-1712	Sequence 1712, Ap

ALIGNMENTS

RESULT 1
US-60-495-114-329
; Sequence 329, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CU001480
; CURRENT APPLICATION NUMBER: US/60/495, 114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 3760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-495-114-329
Alignment Scores:
Pred. No.: 7.68e-71 Length: 3760
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-634-252a-4_COPY_496_599 (1-104) x US-60-495-114-329 (1-3760)
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Db 1709 CCAACAAAGCTATTGAGCCACCGAATGTGAAATGATACGTGGAAGCTGGGAGAG 1768
Qy 21 CysaspCysgllyphenisvalglucyetyrtylglucyCysgllylsyCysSerLeuSer 40

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Db 1769 TGTGATTGTTTTCATGTCGAATGCTGTAAGAAATGTTCCCTCTCC 1828
Qy 41 AaNGlyAlaHieCySeSeraspGlyProCyCySaAsnAntHrSerCysLeuPheGlnPro 60
Db 1829 AACGGGGCTCATTGACAGCCACGGGGCTCTGTACAAATACCTCATGTCTTTTTCAGCCA 1888
Qy 61 ArgGlyTYrGluCyAaArgAspAlaValAaNGluCyAaAspIleThrGluTYrCysThrGly 80
Db 1889 CGAGGGTATGAATGCGGGATGCTGTGAACGAGTGTGATATTACTGAATATTGTACTGGA 1948
Qy 81 AaSPserGlyGlnCySerProProAsnLeuHieSlySGlnAaSPGlyTYrAlaCySaAsnGlnAn 100
Db 1949 GACTCTGGTCAGTGGCCCAATTCCTTCAATACCAAGACGAGATATCATGCAATCAAAAT 2008
Qy 101 GlnGlyArgCys 104
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RESULT 2
US-60-495-114-330
; Sequence 330, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 4071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-495-114-330

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Score: 630.00 Matches: 104
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Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-634-252A-4_COPY_496_599 (1-104) x US-60-495-114-330 (1-4071)
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Qy 21 CysAaSPCySGlyPheHieValGluCySTYrGlyLeuCyAeSlySlySlySerLeuSer 40
Db 1769 TGTGATTGTTTTCATGTCGAATGCTGTAAGAAATGTTCCCTCTCC 1828
Qy 41 AaNGlyAlaHieCySeSeraspGlyProCyCySaAsnAntHrSerCysLeuPheGlnPro 60
Db 1829 AACGGGGCTCATTGACAGCCACGGGGCTCTGTACAAATACCTCATGTCTTTTTCAGCCA 1888
Qy 61 ArgGlyTYrGluCyAaArgAspAlaValAaNGluCyAaAspIleThrGluTYrCysThrGly 80
Db 1889 CGAGGGTATGAATGCGGGATGCTGTGAACGAGTGTGATATTACTGAATATTGTACTGGA 1948
Qy 81 AaSPserGlyGlnCySerProProAsnLeuHieSlySGlnAaSPGlyTYrAlaCySaAsnGlnAn 100
Db 1949 GACTCTGGTCAGTGGCCCAATTCCTTCAATACCAAGACGAGATATCATGCAATCAAAAT 2008
Qy 101 GlnGlyArgCys 104
Db 2009 CAGGGCGGCTGC 2020

RESULT 3
US-60-487-610-948
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; Sequence 948, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 948
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-948

Alignment Scores:
Pred. No.: 4, 83e-42 Length: 1911
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservatve: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: Gaps: 2

US-09-634-252A-4_COPY_496_599 (1-104) x US-60-487-610-948 (1-1911)
Qy 1 ProThrlYleuPheGluProThrGluCySGlyAaNGlyTYrValGlnAaGlyGluGlu 20
Db 1312 CCCCTCAAGCTCTCTGGAGCCCCCAAGTGGCGGAAGGCTTCTGTGAGAGCGAGGAGAG 1371
Qy 21 CysAaSPCySGlyPheHieValGluCySTYr-----GlyLeuCySlySlySlySly 37
Db 1372 TCCGACTCGGCTCGCTCGTCAGAGAGTCAGCCGCGAGGTGGCAATGCTGCAGAAATGC 1431
Qy 38 SerLeuSerAaNGlyAlaHieCySeSeraspGlyProCyCySaAsnAntHrSerCysLeu 57
Db 1432 ACCCTGACTCAGCAGCGCATGTGACGACGCGGCTCTCTGCGCCG-----TGCAG 1485
Qy 58 PheGlnProAaArgGlyTYrGluCyAaArgAspAlaValAaNGluCyAaAspIleThrGluTYr 77
Db 1486 TACGACCAACGCGGGTGTCTCTGCGGAGAGCGCTGAACGAGTGTGACATCGCGGAGACC 1545
Qy 78 CysThrGlyAaSPserGlyGlnCySerProProAsnLeuHieSlySGlnAaSPGlyTYrAlaCys 97
Db 1546 TCCACCGGGAGACTTACGACAGTGGCCGCTTAACCTGCACAAAGCTGAGCGTTACTACTGT 1605
Qy 98 AaNGlnAaNGlnGlyArgCys 104
Db 1606 GACCATGTAGACGAGCGGCTGC 1626

RESULT 4
US-60-485-450-577
; Sequence 577, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 577
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-577
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Alignment Scores:
Pred. No.: 4.83e-42 Length: 1911
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252A-4_COPY_496_599 (1-104) x US-60-485-450-577 (1-1911)

OY 1 ProthrllysleuPhehGupProthrgluCysegllyenglytyrvalaigluaglygluclu 20
Db 1312 CCCCTCAAGCTCTGGACCCCAAGAGTGGCGGAACGGCTTCGTGAGGCGAGGGAGAG 1371
OY 21 CysAspCysegllyPhehlsvalaigluCyseTyr-----GlyLeuCyseLyseLysCys 37
Db 1372 TGGCACTGGCGGTGGGTGCGAGAGTGCAGCCGCCAGGTGGCAATGCTGTCGAAGAAATGC 1411
OY 38 SerleuSeranGlyAlaHisCysSerAspGlyProCyseCysAmaAnthrSerCysleu 57
Db 1432 ACCCTGACTCAGACGCCCATGTGCAGACGCGGCTGTCTGCGTCCG-----TGCAG 1485
OY 58 PheGlnProAspGlyTyrGluCysArgAspAlaValasnGluCysAspIlethrlGluTyr 77
Db 1486 TACCAACACCGGGGTGTCTCTGCGAGAGCGCGTGAACGAGTGCATCGCGAGACC 1545
OY 78 CysThrGlyAspSerGlyGlnCysProProAsnleuHisLysGlnAsnGlyTyrAlaCys 97
Db 1546 TGCACCGGGAGCTTAGCAGTATGCCCGCTTAACCTGCACAAAGCTGACGGTTACTACTGT 1605
OY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1606 GACCATGACGAGCGCGCTGC 1626

RESULT 5

US-60-495-114-825
Sequence 825, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CU001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 825
LENGTH: 3117
TYPE: DNA
ORGANISM: Homo sapiens
US-60-495-114-825

Alignment Scores:
Pred. No.: 9.78e-42 Length: 3117
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252A-4_COPY_496_599 (1-104) x US-60-495-114-825 (1-3117)

OY 1 ProthrllysleuPhehGupProthrgluCysegllyenglytyrvalaigluaglygluclu 20
Db 998 CCCCTCAAGCTCTGGACCCCAAGAGTGGCGGAACGGCTTCGTGAGGCGAGGGAGAG 1057
OY 21 CysAspCysegllyPhehlsvalaigluCyseTyr-----GlyLeuCyseLyseLysCys 37
Db 1058 TGGCACTGGCGGTGGGTGCGAGAGTGCAGCCGCCAGGTGGCAATGCTGTCGAAGAAATGC 1117
OY 38 SerleuSeranGlyAlaHisCysSerAspGlyProCyseCysAmaAnthrSerCysleu 57
Db 1606 GACCATGACGAGCGCGCTGC 1626

Db 1118 ACCCTGACTCAGACGCCCATGTGCAGACGCGGCTGTCTGCGCCG-----TGCAG 1171
OY 58 PheGlnProAspGlyTyrGluCysArgAspAlaValasnGluCysAspIlethrlGluTyr 77
Db 1172 TACCAACACCGGGGTGTCTCTGCGAGAGCGCGTGAACAGATGCGACATCGCGAGACC 1231
OY 78 CysThrGlyAspSerGlyGlnCysProProAsnleuHisLysGlnAsnGlyTyrAlaCys 97
Db 1232 TGCACCGGGAGCTTAGCAGTATGCCCGCTTAACCTGCACAAAGCTGACGGTTACTACTGT 1291
OY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1292 GACCATGACGAGCGCGCTGC 1312

RESULT 6

US-60-487-610-947
Sequence 947, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS.
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 947
LENGTH: 3167
TYPE: DNA
ORGANISM: Homo sapiens
US-60-487-610-947

Alignment Scores:
Pred. No.: 1e-41 Length: 3167
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252A-4_COPY_496_599 (1-104) x US-60-487-610-947 (1-3167)

OY 1 ProthrllysleuPhehGupProthrgluCysegllyAsnGlyTyrvalaigluaglygluclu 20
Db 1312 CCCCTCAAGCTCTGGACCCCAAGAGTGGCGGAACGGCTTCGTGAGGCGAGGGAGAG 1371
OY 21 CysAspCysegllyPhehlsvalaigluCyseTyr-----GlyLeuCyseLyseLysCys 37
Db 1372 TGGCACTGGCGGTGGGTGCGAGAGTGCAGCCGCCAGGTGGCAATGCTGTCGAAGAAATGC 1431
OY 38 SerleuSeranGlyAlaHisCysSerAspGlyProCyseCysAmaAnthrSerCysleu 57
Db 1432 ACCCTGACTCAGACGCCCATGTGCAGACGCGGCTGTCTGCGCCG-----TGCAG 1485
OY 58 PheGlnProAspGlyTyrGluCysArgAspAlaValasnGluCysAspIlethrlGluTyr 77
Db 1486 TACCAACACCGGGGTGTCTCTGCGAGAGCGCGTGAACGAGTGCATCGCGAGACC 1545
OY 78 CysThrGlyAspSerGlyGlnCysProProAsnleuHisLysGlnAsnGlyTyrAlaCys 97
Db 1546 TGCACCGGGAGCTTAGCAGTATGCCCGCTTAACCTGCACAAAGCTGACGGTTACTACTGT 1605
OY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1606 GACCATGACGAGCGCGCTGC 1626
RESULT 7
US-60-485-450-576
Sequence 576, Application US/60485450
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele

```
/ APPLICANT: CHANG, Sheng-Yung
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
/ TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CLO01470
/ CURRENT APPLICATION NUMBER: US/60/485,450
/ CURRENT FILING DATE: 2003-07-09
/ NUMBER OF SEQ ID NOS: 47859
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 576
/ LENGTH: 3167
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-60-485-450-576

Alignment Scores:
Pred. No.: 1e-41 Length: 3167
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-60-485-450-576 (1-3167)
QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTYrValGluAlaGluGlu 20
DB 1312 CCCCTCAAGCTCTGTGAGACCCCGGAGGAGCGGCTTGTGAGGAGGAGGAG 1371
QY 21 CysAspCysGlyPheHisValGluCysTYr-----GlyLeuCysCysLysLysCys 37
DB 1372 TCGCACTCGGCTCGTGCAGAGAGTGCCAGCCGCGCAGCTGCAAGTGTCAAGAAATGC 1431
QY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeu 57
DB 1432 ACCCTGACTCAGCAGCATGTGCAGCAGCGGCTCTGTGTCGCCG-----TGCAG 1485
QY 58 PheGlnProArgGlyTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTYr 77
DB 1486 TACGACCAACGCGGGTGTCTCTCGCGAGAGCGCGTAAAGAGTGCACATCCGCGAGACC 1545
QY 78 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTYrAlaCys 97
DB 1546 TGCACCGGGAGACTGTGACAGTGCAGCGCGCTTAACCTGCACAGTGCAGCTTACTACTGT 1605
QY 98 AsnGlnAsnGlnGlyArgCys 104
DB 1606 GACCATGAGCAGGCGCGCTGC 1626

RESULT 8
US-60-487-610-949
/ Sequence 949, Application US/60487610
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele
/ APPLICANT: HUANG, Hongjin
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INJECTED SUBJECTS,
/ TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO01469
/ CURRENT APPLICATION NUMBER: US/60/487,610
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 97101
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 949
/ LENGTH: 3185
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-60-487-610-949

Alignment Scores:
Pred. No.: 1.01e-41 Length: 3185
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-60-487-610-949 (1-3185)
QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTYrValGluAlaGluGlu 20
DB 1312 CCCCTCAAGCTCTGTGAGACCCCGGAGGAGCGGCTTGTGAGGAGGAGGAG 1371
QY 21 CysAspCysGlyPheHisValGluCysTYr-----GlyLeuCysCysLysLysCys 37
DB 1372 TCGCACTCGGCTCGTGCAGAGAGTGCCAGCGCGCAGCTGCAAGTGTCAAGAAATGC 1431
QY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeu 57
DB 1432 ACCCTGACTCAGCAGCATGTGCAGCAGCGGCTCTGTGTCGCCG-----TGCAG 1485
```

```
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-60-487-610-949 (1-3185)
QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTYrValGluAlaGluGlu 20
DB 1312 CCCCTCAAGCTCTGTGAGACCCCGGAGGAGCGGCTTGTGAGGAGGAGGAG 1371
QY 21 CysAspCysGlyPheHisValGluCysTYr-----GlyLeuCysCysLysLysCys 37
DB 1372 TCGCACTCGGCTCGTGCAGAGAGTGCCAGCGCGCAGCTGCAAGTGTCAAGAAATGC 1431
QY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeu 57
DB 1432 ACCCTGACTCAGCAGCATGTGCAGCAGCGGCTCTGTGTCGCCG-----TGCAG 1485

RESULT 9
US-60-485-450-578
/ Sequence 578, Application US/60485450
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele
/ APPLICANT: CHANG, Sheng-Yung
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
/ TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES
/ FILE REFERENCE: CLO01470
/ CURRENT APPLICATION NUMBER: US/60/485,450
/ CURRENT FILING DATE: 2003-07-09
/ NUMBER OF SEQ ID NOS: 47859
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 578
/ LENGTH: 3185
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-60-485-450-578

Alignment Scores:
Pred. No.: 1.01e-41 Length: 3185
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-60-485-450-578 (1-3185)
QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTYrValGluAlaGluGlu 20
DB 1312 CCCCTCAAGCTCTGTGAGACCCCGGAGGAGCGGCTTGTGAGGAGGAGGAG 1371
QY 21 CysAspCysGlyPheHisValGluCysTYr-----GlyLeuCysCysLysLysCys 37
DB 1372 TCGCACTCGGCTCGTGCAGAGAGTGCCAGCGCGCAGCTGCAAGTGTCAAGAAATGC 1431
QY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeu 57
DB 1432 ACCCTGACTCAGCAGCATGTGCAGCAGCGGCTCTGTGTCGCCG-----TGCAG 1485
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OY 58 PheGlnProArgIYTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyr 77
Db 1486 TACGACCAACGGGGGTGTCTCTCCGAGAGCCCGTGAACGAGTGCAGACATCGCGAGACC 1545
OY 78 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisIleGlnAspGlyTYrAlaCys 97
Db 1546 TGCACCGGGGACTTACGAGTGCAGCCCTTAACCTGCACAGCTGACGGTTACTACTGT 1605
OY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1606 GACCATGACACAGGCCGCTGC 1626

RESULT 10
US-60-495-114-827
; Sequence 827, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CLO01480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 3421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-495-114-827

Alignment Scores:
Pred. No.: 1,12e-41 Length: 3421
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 7 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-60-495-114-827 (1-3421)

OY 1 ProThrIleuLeuPheGlnProThrGluCysGlyAsnGlyTYrValGluAlaGlyGluGlu 20
Db 1312 CCCCTCAGAGCTCTCTGACCCCCAGAGTGCAGGAAAGCGCTTCGTGAGCGAGGAGGAG 1371
OY 21 CysAspCysGlyPheHisValGluCysTYr-----GlyLeuCysCysIleCys 37
Db 1372 TGCAGCTCGGCTCGGTGCAGAGTGCAGCCCGCAGGTGGCACTGCTGCAGAAATGC 1431
OY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysIleu 57
Db 1432 ACCCTGACTCAGACGCGCATGTGCAGCGACGGGCTCTGTCTGCGCGC-----TGCAG 1485
OY 58 PheGlnProArgIYTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyr 77
Db 1486 TACGACCAACGGGGGTGTCTCTCCGAGAGCCCGTGAACGAGTGCAGATCCGCGAGACC 1545
OY 78 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisIleGlnAspGlyTYrAlaCys 97
Db 1546 TGCACCGGGGACTTACGAGTGCAGCCCTTAACCTGCACAGCTGACGGTTACTACTGT 1605
OY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1606 GACCATGACACAGGCCGCTGC 1626

Search completed: October 21, 2003, 14:42:51
Job time : 216.654 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: October 21, 2003, 12:02:06 ; Search time 264.306 Seconds
(without alignments)
1052.855 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630

Sequence: 1 PTKLFETFECEGNGYVEAGE.....CPNHLKQGVACNONGRC 104

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3534790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgnt2_1/USPRO.spool/US09634252/runat_21102003_090327_3499/epi_query.fasta_1.462
-DB=Published.Applications.NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -MATRIX=b10sum2
-TRANS=human40.cdi -DIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=10 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09634252 @CGN 1 1 339 @runat_21102003_090327_3499
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEBUFRY -NEG_SCORES=0 -WAIT -DSELOCK=100
-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA: *
1: /cgnt2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *
2: /cgnt2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq: *
3: /cgnt2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
4: /cgnt2_6/ptodata/1/pubpna/US06_PUBCOMB.seq: *
5: /cgnt2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *
6: /cgnt2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq: *
7: /cgnt2_6/ptodata/1/pubpna/US08_NEW_PUB.seq: *
8: /cgnt2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
9: /cgnt2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq: *
10: /cgnt2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq: *
11: /cgnt2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq: *
12: /cgnt2_6/ptodata/1/pubpna/US09_NEW_PUB.seq: *
13: /cgnt2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *
14: /cgnt2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *
15: /cgnt2_6/ptodata/1/pubpna/US10_NEW_PUB.seq: *
16: /cgnt2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: *
17: /cgnt2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	2268	9	US-09-809-790-1 Sequence 1, Appl1

2	630	100.0	2268	10	US-09-809-617-1	Sequence 1, Appl1
3	630	100.0	2268	12	US-10-260-506-1	Sequence 1, Appl1
4	630	100.0	2499	14	US-10-202-675-2	Sequence 2, Appl1
5	630	100.0	4043	9	US-09-824-129-2	Sequence 2, Appl1
6	630	100.0	4043	12	US-10-359-464-2	Sequence 2, Appl1
7	630	100.0	4720	12	US-10-260-506-9	Sequence 9, Appl1
8	618	98.1	494	11	US-09-918-995-22101	Sequence 22101, A
9	567	90.0	1668	9	US-09-792-2008-17	Sequence 17, Appl1
10	567	90.0	2088	9	US-09-809-790-3	Sequence 3, Appl1
11	567	90.0	2088	10	US-09-809-617-3	Sequence 3, Appl1
12	567	90.0	2088	12	US-10-260-506-3	Sequence 3, Appl1
13	567	90.0	2127	14	US-10-260-506-11	Sequence 11, Appl1
14	363.5	57.7	2604	14	US-10-202-675-5	Sequence 5, Appl1
15	354.5	56.3	494	11	US-09-918-995-2610	Sequence 2610, Ap
16	338.5	53.7	1674	9	US-09-792-2008-15	Sequence 15, Appl1
17	292	46.3	3431	12	US-10-173-308-1	Sequence 1, Appl1
18	292	46.3	3468	12	US-10-177-308-3	Sequence 3, Appl1
19	292	46.3	3582	12	US-10-199-672-465	Sequence 465, App
20	292	46.3	3582	12	US-10-187-749-465	Sequence 465, App
21	292	46.3	3582	12	US-10-194-457-465	Sequence 465, App
22	292	46.3	3582	12	US-10-184-642-465	Sequence 465, App
23	292	46.3	3582	12	US-10-196-747-465	Sequence 465, App
24	292	46.3	3582	12	US-10-173-689-465	Sequence 465, App
25	292	46.3	3582	12	US-10-173-690-465	Sequence 465, App
26	292	46.3	3582	12	US-10-173-691-465	Sequence 465, App
27	292	46.3	3582	12	US-10-173-692-465	Sequence 465, App
28	292	46.3	3582	12	US-10-173-694-465	Sequence 465, App
29	292	46.3	3582	12	US-10-173-698-465	Sequence 465, App
30	292	46.3	3582	12	US-10-173-699-465	Sequence 465, App
31	292	46.3	3582	12	US-10-173-707-465	Sequence 465, App
32	292	46.3	3582	12	US-10-174-569-465	Sequence 465, App
33	292	46.3	3582	12	US-10-174-583-465	Sequence 465, App
34	292	46.3	3582	12	US-10-174-587-465	Sequence 465, App
35	292	46.3	3582	12	US-10-174-589-465	Sequence 465, App
36	292	46.3	3582	12	US-10-174-591-465	Sequence 465, App
37	292	46.3	3582	12	US-10-175-736-465	Sequence 465, App
38	292	46.3	3582	12	US-10-175-742-465	Sequence 465, App
39	292	46.3	3582	12	US-10-175-744-465	Sequence 465, App
40	292	46.3	3582	12	US-10-175-745-465	Sequence 465, App
41	292	46.3	3582	12	US-10-175-748-465	Sequence 465, App
42	292	46.3	3582	12	US-10-175-751-465	Sequence 465, App
43	292	46.3	3582	12	US-10-175-754-465	Sequence 465, App
44	292	46.3	3582	12	US-10-176-480-465	Sequence 465, App
45	292	46.3	3582	12	US-10-176-489-465	Sequence 465, App

ALIGNMENTS

RESULT 1
US-09-809-790-1
Sequence 1, Application US/09809790
Patent No. US20020072102A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Delsner, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/809, 790
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/351, 414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3) ... (2090)
NAME/KEY: misc_feature

LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-809-790-1

Alignment Scores:

Pred. No.: 1,45e-69 Length: 2268
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 9

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-809-790-1 (1-2268)

QY 1 ProthrrlyLeuphegluProthrrlyCysglYasnglyTYrvaIgluAglYglu 20
Db 1119 CCAACAAAGCTATTGGAGCCCGAATGTGAATGATGCTGGAAGCTGGGAGAG 1178
QY 21 CysaapCysglYpnehiVaIgluCystrYglYleuCYsLysLysCysSerleuser 40
Db 1179 TGTGATTGGTTTTCATGTGGAATGCTATGATTTATGTAAGAAATGTTCCCTCC 1238
QY 41 AsnglyIahisCysSerAspGlyProCYsAsanaenThrSerCysleuphegluPro 60
Db 1239 AACGGGCTCAGTGCAGCGAGCGGCCCTGCTTAACAATACCTCAAGTCTTTTCAGCCA 1298
QY 61 ArgglYTYrGlucYsArgAspAlaValAsnglyCysAspIleThrGlutYrCYstrYglY 80
Db 1299 CGAGGTTATGATGCGGGATGCTGTGAACGATGTGATTAAGCAATTTGTAAGTGA 1358
QY 81 AspserGlyGlucYsProProAsnleuHissylsgInaAspGlyTYrAlaCYsAsngInAsn 100
Db 1359 GACTGTGTCAGTGCAGCGCCCAATATCTTCAAGCAAGCGATATGCAATCAATCAAAAT 1418
QY 101 GlnGlyArgCys 104
Db 1419 CAGGGCCGCTGC 1430

RESULT 2

US-09-809-617-1
Sequence 1, Application US/09809617
Patent No. US20020137178A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baird, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/809,617
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US/09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-809-617-1

Alignment Scores:

Pred. No.: 1,45e-69 Length: 2268
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-809-617-1 (1-2268)

QY 1 ProthrrlyLeuphegluProthrrlyCysglYasnglyTYrvaIgluAglYglu 20
Db 1119 CCAACAAAGCTATTGGAGCCCGAATGTGAATGATGCTGGAAGCTGGGAGAG 1178
QY 21 CysaapCysglYpnehiVaIgluCystrYglYleuCYsLysLysCysSerleuser 40
Db 1179 TGTGATTGGTTTTCATGTGGAATGCTATGATTTATGTAAGAAATGTTCCCTCC 1238
QY 41 AsnglyIahisCysSerAspGlyProCYsAsanaenThrSerCysleuphegluPro 60
Db 1239 AACGGGCTCAGTGCAGCGAGCGGCCCTGCTTAACAATACCTCAATGCTTTTCAGCCA 1298
QY 61 ArgglYTYrGlucYsArgAspAlaValAsnglyCysAspIleThrGlutYrCYstrYglY 80
Db 1299 CGAGGTTATGATGCGGGATGCTGTGAACGATGTGATTAAGCAATTTGTAAGTGA 1358
QY 81 AspserGlyGlucYsProProAsnleuHissylsgInaAspGlyTYrAlaCYsAsngInAsn 100
Db 1359 GACTGTGTCAGTGCAGCGCCCAATATCTTCAAGCAAGCGATATGCAATCAATCAAAAT 1418
QY 101 GlnGlyArgCys 104
Db 1419 CAGGGCCGCTGC 1430

RESULT 3

US-10-260-506-1
Sequence 1, Application US/10260506
Publication No. US20030153064A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baird, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
APPLICANT: Taft, David W.
TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
FILE REFERENCE: 98-29C1
CURRENT APPLICATION NUMBER: US/10/260,506
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/092,371
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/147,410
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 09/351,414
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-10-260-506-1

Alignment Scores:

Pred. No.: 1,45e-69 Length: 2268
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-10-260-506-1 (1-2268)


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/ APPLICANT: Miguel, Santiago Cal
/ APPLICANT: Freije, Jose Maria Perez
/ APPLICANT: Garcia, Jose Manuel Lopez
/ APPLICANT: Bianchi, Albert Bernard
/ APPLICANT: Trail, Pamela
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING INTEGRIN-MEDIATED
/ FILE REFERENCE: CELL-CELL INTERACTIONS
/ CURRENT APPLICATION NUMBER: US/10/359,464
/ PRIOR FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: 09/824,129
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: 60/194,164
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 4043
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-359-464-2

Alignment Scores:
Pred. No.: 3,11e-69 Length: 4043
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-10-359-464-2 (1-4043)

QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAlaGluGlu 20
DB 2502 CCAACAACACTATTATAGCCCAACGAAATGTGAAATGATCTGGAAGCTGGAGAGAG 2561

QY 21 CysAspCysGlyPheHisValGluCysTyrGlyLeuCysLysLysCysSerLeuSer 40
DB 2562 TGTGATTGTGTTTTCATGTGAAATGCTATGATTTGCTGTAAAGAAATGTTCCCTCTCC 2621

QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnPro 60
DB 2622 AACGGGGCTCACTGCGACGACGCGGCCCTCTGTAAACAAATCCATCATGTTTTCAGCCA 2681

QY 61 ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIlethnGluTyrCysThrGly 80
DB 2682 CAGGGTATGATATGCGGGATGCTGTAAAGAGATGATTTTCTAAATTTGTTACTGGA 2741

QY 81 AspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsn 100
DB 2742 GACTCTGTCAGTGCACCCCAATCTTCAATAAGCAAGAGATATGCATGCAATCAAAAT 2801

QY 101 GlnGlyArgCys 104
DB 2802 CAGGGCCGCTGC 2813

RESULT 7
US-10-260-506-9
/ Sequence 9, Application US/10260506
/ Publication No. US20030153064A1
/ GENERAL INFORMATION:
/ APPLICANT: Shepard, Paul O.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Deisher, Theresa A.
/ APPLICANT: Bishop, Paul D.
/ APPLICANT: Talt, David W.
/ TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHP
/ FILE REFERENCE: 98-29C1
/ CURRENT APPLICATION NUMBER: US/10/260,506
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: 60/092,371
/ PRIOR FILING DATE: 1998-07-10
/ PRIOR APPLICATION NUMBER: 60/147, 410

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/ PRIOR FILING DATE: 1999-08-05
/ PRIOR APPLICATION NUMBER: 09/351,414
/ PRIOR FILING DATE: 1999-07-09
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 9
/ LENGTH: 4720
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)...(2129)
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(4720)
/ OTHER INFORMATION: n = A,T,C or G
US-10-260-506-9

Alignment Scores:
Pred. No.: 3,83e-69 Length: 4720
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-10-260-506-9 (1-4720)

QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAlaGluGlu 20
DB 1119 CCACAAAGCAATTGTGACCCCAAGAAATGTGAAATGATCTGTGAAGCTGGAGAGAG 1178

QY 21 CysAspCysGlyPheHisValGluCysTyrGlyLeuCysLysLysCysSerLeuSer 40
DB 1179 TGTGATTGTGTTTTCATGTGAAATGCTATGATTTTCTGTAAAGAAATGTTCCCTCTCC 1238

QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnPro 60
DB 1239 AACGGGGCTCACTGCGACGACGCGGCCCTGTGTAAACAAATCATGCTTTTTCAGCCA 1298

QY 61 ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIlethnGluTyrCysThrGly 80
DB 1299 CAGGGTATGATATGCGGGATGCTGTAAAGAGATGATTTTCTAAATTTGTTACTGGA 1358

QY 81 AspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsn 100
DB 1359 GACTCTGTCAGTGCACCCCAATCTTCAATAAGCAAGAGATATGCATGCAATCAAAAT 1418

QY 101 GlnGlyArgCys 104
DB 1419 CAGGGCCGCTGC 1430

RESULT 8
US-09-918-995-22101
/ Sequence 22101, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 22101
/ LENGTH: 494
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature

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LOCATION: (1)...(494)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22101

Alignment Scores:

Pred. No.:	6,296-69	Length:	494
Score:	618.00	Matches:	102
Percent Similarity:	98.08%	Conservative:	0
Best Local Similarity:	98.08%	Mismatches:	2
Query Match:	98.10%	Indels:	0
DB:	11	Gaps:	0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-918-995-22101 (1-494)

Qy 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrrValGluAlaGlyGluGlu 20
Db 126 CCAACAAAGCTATTGAGCCCAACGGAATGTGAAATGATACGTGAAAGCTGGGAGAG 185
Qy 21 CysAspCysGlyPheHisValGluCysTyrrGlyLeuCysGlyValCysSerLeuSer 40
Db 186 TGTGATTGTGCTTTTCATGATGAAATGCTATGATATGCTGTAAATAATGTTCCCTCC 245
Qy 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnThrSerCysLeuPheGluPro 60
Db 246 AACGGGCTCACTGACGACGAGCGCCCTGCTGTAAACAATACCTCAATGCTTTTCAGCCA 305
Qy 61 ArgGlyTyrrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrrCysThrGly 80
Db 306 CGAGGATGATGATGCGGGATGCTGTGACGATCGGATATACGAAATATGTACTGGA 365
Qy 81 AspSerGlyGlnCysProProAsnLeuHisGlyGlnAspGlyTyrrAlaCysAsnGlnAsn 100
Db 366 GACTCTGCTGACGTGCCACCAACATCTTCATAGCAAGACGATAAGCATGCAATCAAAAT 425
Qy 101 GlnGlyArgCys 104
Db 426 CATGCCGCTGC 437

RESULT 9

US-09-792-200B-17
Sequence 17, Application US/09792200B
Patent No. US20020042368A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Fanslow, William C.
APPLICANT: Poindexter, Kurt
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: INTEGRIN ANTAGONISTS
FILE REFERENCE: 2958-A
CURRENT APPLICATION NUMBER: US/09/792,200B
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/184,865
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1668
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion Construct
NAME/KEY: CDS
LOCATION: (25)...(1647)
OTHER INFORMATION:
US-09-792-200B-17

Alignment Scores:

Pred. No.:	3,516-64	Length:	1668
Score:	586.00	Matches:	96
Percent Similarity:	98.97%	Conservative:	0
Best Local Similarity:	98.97%	Mismatches:	1
Query Match:	93.02%	Indels:	0

DB: 9 Gaps: 0
US-09-634-252a-4_COPY_496_599 (1-104) x US-09-792-200B-17 (1-1668)

Qy 8 ThrGluCysGlyAsnGlyTyrrValGluAlaGlyGluGluCysAspCysGlyPheHisVal 27
Db 85 ACTAGTGTGGAATGATGATGCTGAGAGCTGGGAGAGTGTGATGTGTTTCATGTC 144
Qy 28 GluCysTyrrGlyLeuCysCysGlyValCysSerLeuSerAsnGlyAlaHisCysSerAsp 47
Db 145 GAATGCTATGATTTATCTCTGTAAATAATGTTCCCTCTCCACGAGGCTCACTGACGAGAC 204
Qy 48 GlyProCysCysAsnThrSerCysLeuPheGluProArgGlyTyrrGluCysArgAsp 67
Db 205 GGGCCCTGCTGTAAACAATACCTCATGCTTTTCAGCCACGAGGATGATGATGCGGAT 264
Qy 68 AlaValAsnGluCysAspIleThrGluTyrrCysThrGlyAspSerGlyGlnCysProPro 87
Db 265 GCTGTGAACGAGTGTGATTAATGATGATTAATGTAATGTAAGACCTGCTGAGTCCACCA 324
Qy 88 AsnLeuHisGlyGlnAspGlyTyrrAlaCysAsnGlnAsnGlnGlyArgCys 104
Db 325 AATCTTATAGCAAGACGATATGCTGCAATCAAAATCAGGCCCTGC 375

RESULT 10

US-09-809-790-3
Sequence 3, Application US/09809790
Patent No. US20020072102A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Balindur, Nand
APPLICANT: Belsner, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/809,790
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2088
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zdincl amino acid degenerate sequence
NAME/KEY: variation
LOCATION: (1)...(2088)
OTHER INFORMATION: n is any nucleotide
NAME/KEY: misc feature
LOCATION: (1)...(2088)
OTHER INFORMATION:
US-09-809-790-3

Alignment Scores:

Pred. No.:	1,196-61	Length:	2088
Score:	567.00	Matches:	91
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	13
Query Match:	90.00%	Indels:	0
DB:	9	Gaps:	0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-809-790-3 (1-2088)

Qy 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrrValGluAlaGlyGluGlu 20
Db 1117 CCNACNAARYTNTTYTGARCCNACGARTGCGNAAVCGNTAYGTNGARGCNGGARGAR 1176
Qy 21 CysAspCysGlyPheHisValGluCysTyrrGlyLeuCysCysGlyValCysSerLeuSer 40
Db 1177 TGTGATGTGCTTTTCATGATGAAATGCTATGATATGCTGTAAATAATGTTCCCTCC 1236

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Qy      41 AaNGlYAlaHicCySeSeraspGlyProCysCyAsnaSnThrSerCysLeupheGlnPro 60
      1237 AAyGGNGcNCaYtGyWmNGaYGGNCcNTGtGYAAyAAyAACmWmSNTGYtTNTtTYcARcCN 1296
Qy      61 ArgGlyTYrGluCySaRgaSpAlaValaNGluCySaSPlleThrGluTYrCysThrgly 80
      1297 MGNGNTAYGARTGYMGNGAYGCGNGTNAAYGARTGYGAyATHACNGARTAYtGYACNGGN 1356
Qy      81 AspSerGlyGlnCySPProPcAenLeuHlsLyGlnaSPGlyTYrAlaCysaNGlnaSn 100
      1357 GAyWmNGNCARTGYcNCcNcNAyTNCAYAAARcARGAyGNTAYcCNTGYAAyCARAAy 1416
Db      101 GlnGlyArgCys 104
      1417 CARGNMGNtGY 1428

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:27:07 ; Search time 3538.62 Seconds
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Title: US-09-634-252A-4_COPY_496_599
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Ygapop 10.0 , Ygapext 0.5
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=2000000000 -USER=US096334252.0CGN_1_1.5064@runat_21102003_090326_3436
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72: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	630	100.0	2268	27	US-09-631-534-1	Sequence 1, Appl1	
2	630	100.0	2268	34	US-09-809-617-1	Sequence 1, Appl1	
3	630	100.0	2268	34	US-09-809-790-1	Sequence 1, Appl1	
4	630	100.0	2268	49	US-10-260-506-1	Sequence 1, Appl1	
5	630	100.0	2394	40	US-09-949-016-5332	Sequence 5332, Ap	
6	630	100.0	2499	27	US-09-634-252A-2	Sequence 2, Appl1	
7	630	100.0	2499	48	US-10-202-675-2	Sequence 2, Appl1	
8	630	100.0	2899	41	US-10-170-235-22436	Sequence 22436, A	
9	630	100.0	2899	21	US-09-496-321-82	Sequence 82, Appl8	
10	630	100.0	2959	21	US-09-496-321-109	Sequence 109, Appl	
11	630	100.0	2959	65	US-60-118-905-82	Sequence 82, Appl8	
12	630	100.0	2959	65	US-60-118-905-109	Sequence 109, Appl	
13	630	100.0	3054	46	US-10-126-052A-149	Sequence 149, Appl	
14	630	100.0	3054	46	US-10-126-052A-324	Sequence 324, Appl	
15	630	100.0	4043	34	US-09-824-129-2	Sequence 2, Appl1	
16	630	100.0	4043	51	US-10-359-464-2	Sequence 2, Appl1	
17	630	100.0	4440	33	US-09-760-484-15	Sequence 15, Appl8	
18	630	100.0	4720	27	US-09-631-534-9	Sequence 9, Appl1	
19	630	100.0	4720	49	US-10-260-506-9	Sequence 9, Appl1	
20	630	100.0	6391	71	US-60-172-360-21719	Sequence 21719, A	
21	630	100.0	6391	42	US-09-976-594-61	Sequence 61, Appl8	
22	630	100.0	6400	79	US-60-240-409-61	Sequence 61, Appl8	
23	630	100.0	6400	87	US-60-324-185-153	Sequence 1537, Ap	
24	618	98.1	494	17	US-09-234-611-16347	Sequence 16347, A	
25	618	98.1	494	17	US-09-235-076-22101	Sequence 22101, A	
26	618	98.1	494	18	US-09-289-768-220173	Sequence 220173, A	
27	618	98.1	494	19	US-09-332-782-22101	Sequence 22101, A	
28	618	98.1	494	32	US-09-737-223-22101	Sequence 22101, A	
29	618	98.1	494	38	US-09-904-809-16347	Sequence 16347, A	
30	618	98.1	494	38	US-09-918-995-22101	Sequence 22101, A	
31	618	98.1	494	39	US-09-939-397-20173	Sequence 20173, A	
32	617	97.9	6401	75	US-60-213-359-127	Sequence 127, Appl	
33	611	97.0	2271	46	US-10-144-771-15737	Sequence 15737, A	
34	611	97.0	2271	91	US-60-360-207-15373	Sequence 15737, A	
35	586	93.0	1668	33	US-09-792-200C-17	Sequence 17, Appl8	
36	586	93.0	1668	27	US-09-631-534-3	Sequence 3, Appl1	
37	567	90.0	2088	34	US-09-809-617-3	Sequence 3, Appl1	
38	567	90.0	2088	34	US-09-809-617-3	Sequence 3, Appl1	
39	567	90.0	2088	49	US-10-260-506-3	Sequence 3, Appl1	
40	567	90.0	2127	27	US-09-631-534-11	Sequence 11, Appl8	
41	567	90.0	2127	27	US-10-260-506-11	Sequence 11, Appl8	
42	551	87.5	468	22	US-09-519-705-803	Sequence 803, Appl	
43	551	87.5	468	25	US-09-519-455-803	Sequence 803, Appl	
44	551	87.5	468	25	US-10-221-279-792	Sequence 792, Appl	
45	551	87.5	468	48			

ALIGNMENTS

RESULT 1
 US-09-631-534-1
 ; Sequence 1, Application US/09631534
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Balndur, Nand
 ; APPLICANT: Delsher, Theresa A.
 ; APPLICANT: Bishop, Paul D.
 ; APPLICANT: Talc, David W.
 ; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBB
 ; FILE REFERENCE: 98-29c1
 ; CURRENT APPLICATION NUMBER: US/09/631,534
 ; CURRENT FILING DATE: 2000-08-03

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1 PRIOR APPLICATION NUMBER: 60/092,371
2 PRIOR FILING DATE: 1998-07-10
3 PRIOR APPLICATION NUMBER: 60/147, 410
4 PRIOR FILING DATE: 1999-08-05
5 PRIOR APPLICATION NUMBER: 09/351,414
6 PRIOR FILING DATE: 1999-07-09
7 NUMBER OF SEQ ID NOS: 15
8 SOFTWARE: FastSeq for Windows Version 3.0
9 SEQ ID NO 1
10 LENGTH: 2268
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: (3) .. (2090)
16 NAME/KEY: misc_feature
17 LOCATION: (1) .. (12268)
18 OTHER INFORMATION: n = A,T,C or G
19 US-09-631-534-1

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Alignment Scores:

Pred. No.:	4,42e-52	Length:	2266
Score:	630.00	Matches:	104
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-634-252A-4_COPY_496_599 (1-104) X US-09-631-534-1 (1-2268)

QY 1 ProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGluAlaGlyGlu 20

Db 1119 CCACACAAGCTATTGAGCCACGGAATGTGGAATGATACCTGGAAGCTGGGAGAG 1178

21 CysAspCysGlyPheHisValGluCysSTyrGlyLeuCysCysLysLysCysSerLeuSer 40

Db . 1179 TGTGATTGTGTTTTCATGTGGAATGCTATGGAATTATGCTGCTAAGAATGTTCCCTCTCC 1238

41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnPro 60

Db 1239 AACGGGCTCACTGCAGCGACGGGCCCTGCTGTACAATACCTCATGTCTTTTCAGCCA 1298

61 ArgGlyTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTYrCysThrGly 80

Db 1299 CGAGGTATGAATGCCGGATCCTGTGAACGAGTGTGATATTACTGATATTGTACTGGA 1358

81 AspSerGlyIncysProProAsnLeuHisLysGlnAspGlyTyrAlaCysAsnGlnAsn 100

Db 1359 GACTCTGGTCAGTGCCCAATCTTCATAAGCAAGACGGATATGCATGCAATCAAAT 1418

QY 101 GINGIYARGCys 104

D_b 1419 CAGGGCCGCTGC 1430

RESULT 2
116 00 000 017 1

: Sequence 1, Application US/09809617
CURRENT INFORMATION

APPLICANT: Sheppard, Paul O.

APPLICANT: Deisher, Theresa A.

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CURRENT APPLICATION NUMBER: US/09/809,617

PRIOR APPLICATION NUMBER: US/09/351,414

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; NUMBER OF SEQ ID NOS: 13.

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; SEQ ID NO 1
TGGCTT 0000

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;      TYPE: DNA

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)-(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-809-617-1

Alignment Scores:
Pred. No.: 4,42e-52 Length: 2268
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 34 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-809-617-1 (1-2268)

QY 1 ProThrlYsLeuPheGluProThrGluCySGlYAsnGlyTYrValGluAlaGlyGluGlu 20
Db 1119 CCAACAAAGCTATTGAGCCACGGAATGTGAATGATACGTGAAGCTGGGAGAG 1178
QY 21 CyAspCySGlYPhelHsValGluCyTYrGlyLeuCySylYslyCySserLeuSer 40
Db 1179 TGTGATTGTGTTTTCATGTGGAATGCTATGATTATGCTGTAGAAATGTTCCCTCTCC 1238
QY 41 AsnGlyAlaHicYsSerAspGlyProCySAsnAsnThrSerCylsLeuPheGlnPro 60
Db 1239 AACGGGCTCTACCTGACGAGCGGCGCTGCTGTACCAATACCTATGCTTTTCACCCA 1298
QY 61 ArgGlyTYrGluCySArGAspAlaValAsnGluCyAspIleThrGluTYrCySThrGly 80
Db 1299 CGAGGATATGAATCCCGGAGTGTGTGAACGAGTGTATTAATTAATTTGACTGGA 1358
QY 81 AspSerGlyGlnCySProProAsnLeuHslySGlnAspGlyTYrAlaCySAsnGlnAsn 100
Db 1359 GACTCTGTGTCAGTCCACCAAAATCTTCATAGCAAGCGATATGATCAATCAAAAT 1418
QY 101 GlnGlyArGcys 104
Db 1419 CAGGGCCGCTGC 1430

RESULT 3

US-09-809-790-1
Sequence 1, Application US/09809790
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/809,790
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)-(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-809-790-1

Alignment Scores:
Pred. No.: 4,42e-52 Length: 2268

Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 34 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-809-790-1 (1-2268)

QY 1 ProThrlYsLeuPheGluProThrGluCySGlYAsnGlyTYrValGluAlaGlyGluGlu 20
Db 1119 CCAACAAAGCTATTGAGCCACGGAATGTGAATGATACGTGAAGCTGGGAGAG 1178
QY 21 CyAspCySGlYPhelHsValGluCyTYrGlyLeuCySylYslyCySserLeuSer 40
Db 1179 TGTGATTGTGTTTTCATGTGGAATGCTATGATTATGCTGTAGAAATGTTCCCTCTCC 1238
QY 41 AsnGlyAlaHicYsSerAspGlyProCySAsnAsnThrSerCylsLeuPheGlnPro 60
Db 1239 AACGGGCTCTACCTGACGAGCGGCGCTGCTGTACCAATACCTATGCTTTTCACCCA 1298
QY 61 ArgGlyTYrGluCySArGAspAlaValAsnGluCyAspIleThrGluTYrCySThrGly 80
Db 1299 CGAGGATATGAATCCCGGAGTGTGTGAACGAGTGTATTAATTAATTTGACTGGA 1358
QY 81 AspSerGlyGlnCySProProAsnLeuHslySGlnAspGlyTYrAlaCySAsnGlnAsn 100
Db 1359 GACTCTGTGTCAGTCCACCAAAATCTTCATAGCAAGCGATATGATCAATCAAAAT 1418
QY 101 GlnGlyArGcys 104
Db 1419 CAGGGCCGCTGC 1430

RESULT 4

US-10-260-506-1
Sequence 1, Application US/10260506
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Taft, David W.
TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
FILE REFERENCE: 98-29C1
CURRENT APPLICATION NUMBER: US/10/260,506
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/092,371
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/147,410
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)-(2268)
OTHER INFORMATION: n = A,T,C or G
US-10-260-506-1

Alignment Scores:
Pred. No.: 4,42e-52 Length: 2268
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 49 Gaps: 0

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US-09-634-252a-4_COPY_496_599 (1-104) x US-10-260-506-1 (1-2268)
QY 1 ProthrlvsleuphegluProthrgluCysglsyAsnglyTYrValgluIaaglglu 20
Db 1119 CCACAAAGCTATTGAGCCCAAGGAATGGAATGATGGAACCTGGAGAG 1178
QY 21 CysaspCysglsyPhehisValgluCyTYrTglYleuCyCyslylsyCysSerleuser 40
Db 1179 TGTGATGTGCTTTCATGATGGAATGCTATGATTATGCTGTAAGAAATGTTCCCTCTCC 1238
QY 41 AenglyAlahisCysSerleuserProCysCysAsnAntHserCysleuphegluPro 60
Db 1239 AACGGGGCTCAGTCGACGACGAGCGGCCCTCTGTAACAAATCCTCATGCTTTTCAGCCA 1298
QY 61 ArgglyTYrGluCysArgaspAlaValAsngluCysAspIleThrgluTYrCysThrgly 80
Db 1299 CAGGGTATGAAATGCCGGATGCTGTGAACGATGATTAATGTAATGTAATGTAATGTA 1358
QY 81 AspserglyGlnCysProProAsnleuHislysglnAspIleTYrAlaCysAsnglnAsn 100
Db 1359 GACTCTGTCAGTGCACGACCAATCTTCTAATAGCAAGGATATGCAATCAAAAT 1418
QY 101 GlnGlyArgCys 104
Db 1419 CAGGGCCGCTGC 1430

RESULT 5
US-09-949-016-5332
; Sequence 5332, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5332
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5332

Alignment Scores:
Pred. No.: 4 71e-52 Length: 2394
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-949-016-5332 (1-2394)
QY 1 ProthrlvsleuphegluProthrgluCysglsyAsnglyTYrValgluIaaglglu 20
Db 1050 CCACAAAGCTATTGAGCCCAAGGAATGGAATGATGGAACCTGGAGAG 1109
QY 21 CysaspCysglsyPhehisValgluCyTYrTglYleuCyCyslylsyCysSerleuser 40
Db 1110 TGTGATGTGCTTTCATGATGGAATGCTATGATTATGCTGTAAGAAATGTTCCCTCTCC 1169
QY 41 AenglyAlahisCysSerleuserProCysCysAsnAntHserCysleuphegluPro 60
Db 1170 AACGGGGCTCAGTCGACGACGAGCGGCCCTCTGTAACAAATCCTCATGCTTTTCAGCCA 1229
```

```
QY 61 ArgglyTYrGluCysArgaspAlaValAsngluCysAspIleThrgluTYrCysThrgly 80
Db 1230 CAGGGTATGAAATGCCGGATGCTGTGAACGATGATTAATGTAATGTAATGTAATGTA 1289
QY 81 AspserglyGlnCysProProAsnleuHislysglnAspIleTYrAlaCysAsnglnAsn 100
Db 1290 GACTCTGTCAGTGCACCAAAATCTTCTAATAGCAAGGATATGCAATCAAAAT 1349
QY 101 GlnGlyArgCys 104
Db 1350 CAGGGCCGCTGC 1361

RESULT 6
US-09-634-252a-2
; Sequence 2, Application US/09634252A
; GENERAL INFORMATION:
; APPLICANT: Coriell, Douglas P.
; TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES
; FILE REFERENCE: 03260.0051-00304
; CURRENT APPLICATION NUMBER: US/09/634,252A
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/074,310
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-634-252a-2

Alignment Scores:
Pred. No.: 4.95e-52 Length: 2499
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-634-252a-2 (1-2499)
QY 1 ProthrlvsleuphegluProthrgluCysglsyAsnglyTYrValgluIaaglglu 20
Db 1486 CCACAAAGCTATTGAGCCCAAGGAATGGAATGATGGAACCTGGAGAG 1545
QY 21 CysaspCysglsyPhehisValgluCyTYrTglYleuCyCyslylsyCysSerleuser 40
Db 1546 TGTGATGTGCTTTCATGATGGAATGCTATGATTATGCTGTAAGAAATGTTCCCTCTCC 1605
QY 41 AenglyAlahisCysSerleuserProCysCysAsnAntHserCysleuphegluPro 60
Db 1606 AACGGGGCTCAGTCGACGACGAGCGGCCCTCTGTAACAAATCCTCATGCTTTTCAGCCA 1665
QY 61 ArgglyTYrGluCysArgaspAlaValAsngluCysAspIleThrgluTYrCysThrgly 80
Db 1666 CAGGGTATGAAATGCCGGATGCTGTGAACGATGATTAATGTAATGTAATGTAATGTA 1725
QY 81 AspserglyGlnCysProProAsnleuHislysglnAspIleTYrAlaCysAsnglnAsn 100
Db 1726 GACTCTGTCAGTGCACCAAAATCTTCTAATAGCAAGGATATGCAATCAAAAT 1785
QY 101 GlnGlyArgCys 104
Db 1786 CAGGGCCGCTGC 1797

RESULT 7
US-10-202-675-2
; Sequence 2, Application US/10202675
; GENERAL INFORMATION:
; APPLICANT: Coriell, Douglas P.
; TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES
; FILE REFERENCE: 03260.0051-00304
; CURRENT APPLICATION NUMBER: US/10/202,675
```


CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US/09/634,252
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/074,310
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 2499
TYPE: DNA
ORGANISM: Homo sapiens
US-10-202-675-2

Alignment Scores:
Pred. No.: 4,95e-52 Length: 2499
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 48 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-10-202-675-2 (1-2499)

QY 1 Prothrllysleuphegluprothrnglucysglaasnlytyryvalglualaglglglu 20
Db 1486 CCAACAAAGCTATTGTGAGCCACGGAATGTGAATGATACGTGAAGCTGGGAGAG 1545

QY 21 CysaspCysglYpHehIsvaIGlucYstYrGlYleucYsSlylylYsCysSerleuSer 40
Db 1546 TGTGATTGTGTTTTCATGTGGAATGCTATGATTTGCTTAAGAAATGTTCCCTCC 1605

QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAnthrSerCysLeupheglupro 60
Db 1606 AACGGGCTCACTGACGAGGAGCGGCGCTGTAAACATACCTCTGCTTTTCAGCA 1665

QY 61 ArgGlyTyrglucYsaTgaAspAlaValAsnGlucYsaSppIleThrglYrCysThrgly 80
Db 1666 CGAGGATGATGATCCGGGATGCTGTGAACAGATGTGATTAAGATATTGACTGGA 1725

QY 81 AspserGlyInCysProProAsnLeuHisIlysgInAspGlyTyryAlaCysAsnGlnasn 100
Db 1726 GACTCTGTGATGCTGACCCCAAAATCTTCAATAAGCAAGGATATGCAATCAAAAT 1785

QY 101 GlnGlyArgCys 104
Db 1786 CAGGGCCGCTGC 1797

RESULT 8
US-10-170-235-22436
Sequence 22436, Application US/10170235
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CLO01380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 22436
LENGTH: 2899
TYPE: DNA
ORGANISM: HUMAN
US-10-170-235-22436

Alignment Scores:
Pred. No.: 5.88e-52 Length: 2899
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 47 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-10-170-235-22436 (1-2899)

QY 1 Prothrllysleuphegluprothrnglucysglaasnlytyryvalglualaglglglu 20
Db 1555 CCAACAAAGCTATTGTGAGCCACGGAATGTGAATGATACGTGAAGCTGGGAGAG 1614

QY 21 CysaspCysglYpHehIsvaIGlucYstYrGlYleucYsSlylylYsCysSerleuSer 40
Db 1615 TGTGATTGTGTTTTCATGTGGAATGCTATGATTTGCTTAAGAAATGTTCCCTCC 1674

QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAnthrSerCysLeupheglupro 60
Db 1675 AACGGGCTCACTGACGAGGAGCGGCGCTGTAAACATACCTCATGCTTTTCAGCCA 1734

QY 61 ArgGlyTyrglucYsaTgaAspAlaValAsnGlucYsaSppIleThrglYrCysThrgly 80
Db 1735 CGAGGATGATGATCCGGGATGCTGTGAACAGATGATATTGATGATGGA 1794

QY 81 AspserGlyInCysProProAsnLeuHisIlysgInAspGlyTyryAlaCysAsnGlnasn 100
Db 1795 GACTCTGTGATGCTGACCCCAAAATCTTCAATAAGCAAGGATATGCAATCAAAAT 1854

QY 101 GlnGlyArgCys 104
Db 1855 CAGGGCCGCTGC 1866

RESULT 9
US-09-496-321-82
Sequence 82, Application US/09496321
GENERAL INFORMATION:
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING RECEPTOR PROTEINS
FILE REFERENCE: PA-0014 US
CURRENT APPLICATION NUMBER: US/09/496,321
CURRENT FILING DATE: 2000-02-01
EARLIER APPLICATION NUMBER: 60/118,905
EARLIER FILING DATE: February 5, 1999
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PERL Program
SEQ ID NO 82
LENGTH: 2959
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 305461
US-09-496-321-82

Alignment Scores:
Pred. No.: 6.03e-52 Length: 2959
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-496-321-82 (1-2959)

QY 1 Prothrllysleuphegluprothrnglucysglaasnlytyryvalglualaglglglu 20
Db 426 CCAACAAAGCTATTGTGAGCCACGGAATGTGAATGATACGTGAAGCTGGGAGAG 485.

QY 21 CysaspCysglYpHehIsvaIGlucYstYrGlYleucYsSlylylYsCysSerleuSer 40
Db 486 TGTGATTGTGTTTTCATGTGGAATGCTATGATTTGCTTAAGAAATGTTCCCTCC 545

QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAnthrSerCysLeupheglupro 60
Db 546 AACGGGCTCACTGACGAGGAGCGGCGCTGTGAACATACCTCATGCTTTTCAGCCA 605

QY 61 ArgGlyTyrglucYsaTgaAspAlaValAsnGlucYsaSppIleThrglYrCysThrgly 80
Db 606 CGAGGATGATGATCCGGGATGCTGTGAACAGATGATATTGATGATGATGGA 665

QY 81 AspSerGlyGlnCysProProAsnLeuHisIleValGlnAspGlyTyrAlaCysAsnGlnAsn 100
 DB 666 GACTCTGGTCAGTGGCCCAACAAATCTTCAATAGCAAGACGATATGCATGCAATCAAAAT 725
 QY 101 GINGLYARGCys 104
 DB 726 CAGGGCCGCTGC 737

RESULT 10

US-09-496-321-109
 ; Sequence 109, Application US/09496321
 ; GENERAL INFORMATION:
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Guegler, Karl, J.
 ; APPLICANT: Au-Young, Janice
 ; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING RECEPTOR PROTEINS
 ; FILE REFERENCE: PA-0014 US
 ; CURRENT APPLICATION NUMBER: US/09/496,321
 ; CURRENT FILING DATE: 2000-02-01
 ; EARLIER APPLICATION NUMBER: 60/118,905
 ; EARLIER FILING DATE: February 5, 1999
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 109
 ; LENGTH: 2959
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: -
 ; OTHER INFORMATION: 3859516
 US-09-496-321-109

Alignment Scores:

Pred. No.: 6, 03e-52 Length: 2959
 Score: 630.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-634-252a-4_copy_496_599 (1-104) x US-09-496-321-109 (1-2959)

QY 1 ProThrIleValLeuPheGluProThrGluCysGlyAsnGlyTyrValGlnAlaGlyGlu 20
 DB 426 CCAACAAAGCTATTGAGCCCAACGAATGTGAAATGATACGTGAAAGCTGGGAGAG 485
 QY 21 CysAspCysGlyPheHisValGlnCysTyrGlyLeuCysCysIleValCysSerLeuSer 40
 DB 486 TGTGATTGTGGTTTTCATGTGAAATGCTAAGGATTATGCTGTAGAAATGTTCCCTCTCC 545
 QY 41 AsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCysLeuPheGlnPro 60
 DB 546 AACGGGGCTCAGTCGACGACGCGGCCCTCTGTAAACATACCTCATGCTTTTTCAGCCA 605
 QY 61 ArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyrCysThrGly 80
 DB 606 CAGGGGTATGAATGCGGGATGCTGTGAACGAGTGTATTACTGAATATTGTACTGGA 665
 QY 81 AspSerGlyGlnCysProProAsnLeuHisIleValGlnAspGlyTyrAlaCysAsnGlnAsn 100
 DB 666 GACTCTGGTCAGTGGCCCAACAAATCTTCAATAGCAAGACGATATGCATGCAATCAAAAT 725
 QY 101 GINGLYARGCys 104
 DB 726 CAGGGCCGCTGC 737

Search completed: October 21, 2003, 14:37:17
 Job time : 3546.62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:08:40 ; Search time 17.6604 Seconds
(without alignments)
190.928 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTKLFEPTGCGNGYVGEAGE.....CPPLHKQDGVACNONGRC 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 153893 seqs, 32421815 residues

Total number of hits satisfying chosen parameters: 153893

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCIT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	832	7	US-60-495-114-1465 Sequence 1465, Ap
2	630	100.0	832	7	US-60-495-114-1466 Sequence 1466, Ap
3	404.5	64.2	369	7	US-60-495-114-1961 Sequence 1961, Ap
4	404.5	64.2	623	7	US-60-487-610-2361 Sequence 2361, Ap
5	404.5	64.2	623	7	US-60-485-450-1482 Sequence 1482, Ap
6	404.5	64.2	623	7	US-60-495-114-1962 Sequence 1962, Ap
7	404.5	64.2	769	7	US-60-487-610-2360 Sequence 2360, Ap
8	404.5	64.2	769	7	US-60-485-450-1481 Sequence 1481, Ap
9	404.5	64.2	769	7	US-60-495-114-1963 Sequence 1963, Ap
10	404.5	64.2	773	7	US-60-495-114-1964 Sequence 1964, Ap
11	404.5	64.2	775	7	US-60-487-610-2362 Sequence 2362, Ap
12	404.5	64.2	775	7	US-60-485-450-1483 Sequence 1483, Ap
13	363.5	57.7	761	7	US-60-495-114-1301 Sequence 1301, Ap
14	363.5	57.7	761	7	US-60-495-114-1302 Sequence 1302, Ap
15	363.5	57.7	823	7	US-60-490-890-1043 Sequence 1043, Ap
16	363.5	57.7	823	7	US-60-495-114-1304 Sequence 1304, Ap
17	363.5	57.7	823	7	US-60-495-114-1309 Sequence 1309, Ap
18	363.5	57.7	853	7	US-60-495-114-1310 Sequence 1310, Ap
19	363.5	57.7	859	7	US-60-490-890-1039 Sequence 1039, Ap
20	363.5	57.7	864	7	US-60-495-114-1308 Sequence 1308, Ap
21	363.5	57.7	870	7	US-60-490-890-1041 Sequence 1041, Ap
22	363.5	57.7	870	7	US-60-495-114-1305 Sequence 1305, Ap
23	363.5	57.7	870	7	US-60-495-114-1311 Sequence 1311, Ap
24	363.5	57.7	893	7	US-60-495-114-1307 Sequence 1307, Ap
25	363.5	57.7	899	7	US-60-495-114-1303 Sequence 1303, Ap
26	363.5	57.7	899	7	US-60-495-114-1306 Sequence 1306, Ap

27	363.5	57.7	900	7	US-60-495-114-1312 Sequence 1312, Ap
28	292	46.3	746	6	US-10-670-184-4 Sequence 4, Appl
29	292	46.3	787	6	PCT-US03-30720-951 Sequence 951, Appl
30	292	46.3	787	6	US-10-670-184-5 Sequence 5, Appl
31	292	46.3	787	7	US-60-495-114-2100 Sequence 2100, Ap
32	292	46.3	813	7	US-60-495-114-2101 Sequence 2101, Ap
33	292	46.3	824	1	PCT-US03-28227-4610 Sequence 4610, Ap
34	292	46.3	824	1	PCT-US03-28227-4612 Sequence 4612, Ap
35	292	46.3	840	1	PCT-US03-30720-1275 Sequence 1275, Ap
36	292	46.3	849	6	US-10-670-184-6 Sequence 6, Appl
37	292	46.3	863	1	PCT-US03-28227-4611 Sequence 4611, Ap
38	274	43.5	356	7	US-60-495-114-1584 Sequence 1584, Ap
39	274	43.5	358	1	PCT-US03-26780-1448 Sequence 1448, Ap
40	274	43.5	409	7	US-60-495-114-1583 Sequence 1583, Ap
41	274	43.5	652	7	US-60-495-114-1585 Sequence 1585, Ap
42	274	43.5	778	7	US-60-487-610-1926 Sequence 1926, Ap
43	274	43.5	781	7	US-60-487-610-1924 Sequence 1924, Ap
44	274	43.5	802	7	US-60-487-610-1925 Sequence 1925, Ap
45	274	43.5	814	1	PCT-US03-28751-4 Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-60-495-114-1465
; Sequence 1465, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1465
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1465

Query Match      100.0%: Score 630; DB 7; Length 832;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PTKLFEPTGCGNGYVGEAGECDGPFHVECYGLCKKCSLSNGAHCSDGPPCCNNTSCUFOP 60
Db      496 PTKLFEPTGCGNGYVGEAGECDGPFHVECYGLCKKCSLSNGAHCSDGPPCCNNTSCUFOP 555

QY      61 RGVECRDANVECDITTEYCTGDSGCGCPNHLHKQGYACNONGRC 104
Db      556 RGVECRDANVECDITTEYCTGDSGCGCPNHLHKQGYACNONGRC 599

RESULT 2
US-60-495-114-1466
; Sequence 1466, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1466
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-60-495-114-1466

Query Match	100.0%;	Score 630;	DB 7;	Length 832;
Best Local Similarity	100.0%;	Pred. No. 1.5e-20;		
Matches 104;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	PTLTFEETEGCGNVVEAGEECDCGCFVHECYGLCKCKKSLSNNAHSDGPCNNTCLPQF	60
DQ	496	PTLTFEETEGCGNVVEAGEECDCGCFVHECYGLCKCKKSLSNNAHSDGPCNNTCLPQF	555
QY	61	RGVECDPAVNECDITETCTGDSGCGCPNIAHKDGYACNONGRC	104
DQ	556	RGVECDPAVNECDITETCTGDSGCGCPNIAHKDGYACNONGRC	599

RESULT 3
US-60-495-114-1961

```

: Sequence 1961, Application US/60495114
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
: TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: C0001480
: CURRENT APPLICATION NUMBER: US/60/495,114
: CURRENT FILING DATE: 2003-08-15
: NUMBER OF SEQ ID NOS: 91238
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1961
: LENGTH: 369
: TYPE: PRF
: ORGANISM: Homo sapiens
US-60-495-114-1961

```

Query Match	64.2%;	Score 404.5;	DB 7;	Length 369;
Best Local Similarity	65.4%;	Pred. No. 2.4e-11;		
Matches 70; Conservative	9;	Mismatches 23;	Indels 5	

QY 1 PTKLFEPTGCGNGYVEAGEECDCGFHECY---GLCKCKCSLSNGAHSDDPCCNNTSL 57
||| : ||||| : ||||| : ||||| :
Db 184 PLKLIDPPEGCGFVAGEECCDGSVGECSRAGNCKCKCTLTHDAMCSDGLCRR--CK 241

RESULT 4
US-60-487-610-2361

```

: Sequence 2361, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS.
: TITLE OF INVENTION: METHODS OF DETECTION AND USE THEREOF
: FILE REFERENCE: C0001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2361
: LENGTH: 623
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-60-487-610-2361

```

Query Match	64.2%	Score 404.5;	DB 7;	Length 623;
Best Local Similarity	65.4%	Pred. No. 3.4e-11;		
Matches 70; Conservative	9;	Mismatches 23;	Indels 5;	Gaps 2

QY 1 PTKLFETECNGYVEAGHECDGFHVECT--GLCCCKSLSNAGHCSDDGPCCNTTSCL 5

Db 438 PLKLDPECGNFVEAGEECDGSGVQEC SRAGNCKKCTLTHDAMCS DGLCCR--CK 495

```
QY      58  FQPRGYECRDVAVNECDITEYCTGSGGCPPLNLHKQDGYACNQNGRC 104
      ::||| ||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      496  YEPRGVSCREAVNECDIAETCTGTGSSQCPPLNLHKLKLDGYCDHEQGR 542
```

RESULT 5
US-60-485-450-1482
: Sequence 1482, Application US/60485450

```

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THERSOF
FILE REFERENCE: C1001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1482
LENGTH: 623
TYPE: PRF
ORGANISM: Homo sapiens
US-60-485-450-1482

```

Query Match	64.2%	Score 404.5;	DB 7;	Length 623;
Best Local Similarity	65.4%;	Pred. No. 3.4e-11;		
Matches 70; Conservative	9;	Mismatches 23;	Indels 5;	Gaps 2

QY 1 PTKLFETTECGNGVGEAGEEDCCGFHYECY----GLCKCGLSSNGAHGSDSPCCNNTSCL 57
Db 438 PLKLLDPECGNGVGEAGEEDCGSVGECRAGNCCCKCTLTLDAMCSDSLCCRR--CK 495

QY 58 FQPRGYCRDAVNECDITETCTGSGGQCPPLHLKQDGYACNQNGRC 104
Db 496 YEPGVGSCREAVNECDLAEITCTGSSQCPPLHLKLDGYVCDHEGRC 542

RESULT 6
US-60-495-114-1962
; Sequence 1962, Application US/60495114
; GENERAL INFORMATION:

```

: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
: TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CLO01480
: CURRENT APPLICATION NUMBER: US/60/495,114
: CURRENT FILING DATE: 2003-08-15
: NUMBER OF SEQ ID NOS: 91238
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1962
: LENGTH: 623
: TYPE: prt
: ORGANISM: Homo sapiens
: OS-60-495-114-1962

```

Query Match	64.2%;	Score 404.5;	DB 7;	Length 623;
Best Local Similarity	65.4%;	Pred. No. 3.4e-11;		
Matches 70; Conservative	9;	Mismatches 23;	Indels 5;	Gaps 2;

DQ
1 PTLFEPHEGCGVVEAGEECDGCHVECY--GLCKKCSLSNGAHCSDDGCCNNNSCL 57
||| : ||||| : ||||| : ||||| : ||||| :
Dd 438 PLKLDPREGCGVFEAGEECDGCVQECRAGANGCKKCTLTLDAMCSDGLCCRR--CK 495

QY 58 FQPRGYECRDVAINECDITEYCTGSGGCCPRLNHLKQDGYACNNQNGRC 104
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 496 YEPRGVSCREAVNECDIAETCTGSSQCPRNLHKLDDGYCDHEQGRC 542

```
RESULT 7
US-60-487-610-2360
; Sequence 2360, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2360
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2360

Query Match          64.2%; Score 404.5; DB 7; Length 769;
Best Local Similarity 65.4%; Pred. No. 3.8e-11;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECY---GLCKKCSLSNGAHCSGDPCCNNTSCL 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 438 PLKLDPEPCGNGFVEAGEECDCGSGVQECSRAGNCKKCTLTTHDAMCSDDLCCRR--CK 495

Qy 58 FQPRGYECRDVAINECDITETCTGDSGCGPPNLHKODGYACNONGRC 104
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 496 YEPRGVSCREAVNECDIAETCTGDSGCGPPNLHKLDGYCDHEGRC 542

RESULT 8
US-60-485-450-1481
; Sequence 1481, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1481
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1481

Query Match          64.2%; Score 404.5; DB 7; Length 769;
Best Local Similarity 65.4%; Pred. No. 3.8e-11;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECY---GLCKKCSLSNGAHCSGDPCCNNTSCL 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 438 PLKLDPEPCGNGFVEAGEECDCGSGVQECSRAGNCKKCTLTTHDAMCSDDLCCRR--CK 495

Qy 58 FQPRGYECRDVAINECDITETCTGDSGCGPPNLHKODGYACNONGRC 104
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 496 YEPRGVSCREAVNECDIAETCTGDSGCGPPNLHKLDGYCDHEGRC 542

RESULT 9
US-60-495-114-1963
; Sequence 1963, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
```

```
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1963
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1963

Query Match          64.2%; Score 404.5; DB 7; Length 769;
Best Local Similarity 65.4%; Pred. No. 3.8e-11;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECY---GLCKKCSLSNGAHCSGDPCCNNTSCL 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 438 PLKLDPEPCGNGFVEAGEECDCGSGVQECSRAGNCKKCTLTTHDAMCSDDLCCRR--CK 495

Qy 58 FQPRGYECRDVAINECDITETCTGDSGCGPPNLHKODGYACNONGRC 104
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 496 YEPRGVSCREAVNECDIAETCTGDSGCGPPNLHKLDGYCDHEGRC 542

RESULT 10
US-60-495-114-1964
; Sequence 1964, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1964
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1964

Query Match          64.2%; Score 404.5; DB 7; Length 773;
Best Local Similarity 65.4%; Pred. No. 3.8e-11;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECY---GLCKKCSLSNGAHCSGDPCCNNTSCL 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 438 PLKLDPEPCGNGFVEAGEECDCGSGVQECSRAGNCKKCTLTTHDAMCSDDLCCRR--CK 495

Qy 58 FQPRGYECRDVAINECDITETCTGDSGCGPPNLHKODGYACNONGRC 104
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 496 YEPRGVSCREAVNECDIAETCTGDSGCGPPNLHKLDGYCDHEGRC 542

Search completed: October 21, 2003, 10:21:22
Job time : 18.6604 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:06:10 ; Search time 314.616 Seconds
(without alignments)
300.784 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTLFEPTECGNGYVAGEE.....CPNLHKDGVACHONGRC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA Main:*

- 1: /cgn2_6/ptodata/2/paa/PCRTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
- 17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
- 18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US099A_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US099B_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 27: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 28: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
- 29: /cgn2_6/ptodata/2/paa/US103_COMB.pep.*
- 30: /cgn2_6/ptodata/2/paa/US104_COMB.pep.*
- 31: /cgn2_6/ptodata/2/paa/US106_COMB.pep.*
- 32: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	686	24	US-09-949-016-11203
					Sequence 11203, A

2	630	100.0	696	20	US-09-631-534-2	Sequence 2, App1
3	630	100.0	696	23	US-09-809-617-2	Sequence 2, App1
4	630	100.0	696	23	US-09-809-790-2	Sequence 2, App1
5	630	100.0	696	28	US-10-260-506-2	Sequence 2, App1
6	630	100.0	709	20	US-09-631-534-10	Sequence 10, App1
7	630	100.0	709	28	US-10-260-506-10	Sequence 10, App1
8	630	100.0	776	22	US-09-760-484-315	Sequence 315, App
9	630	100.0	832	22	US-09-634-252a-4	Sequence 4, App1
10	630	100.0	832	22	US-09-791-537-64795	Sequence 64795, A
11	630	100.0	832	27	US-10-126-052a-150	Sequence 3, App1
12	630	100.0	832	27	US-10-126-052a-150	Sequence 150, App
13	630	100.0	832	27	US-10-126-052a-150	Sequence 125, App
14	630	100.0	832	27	US-10-126-052a-150	Sequence 4, App1
15	630	100.0	832	29	US-10-359-464-3	Sequence 3, App1
16	611	97.0	829	22	US-09-791-537-142799	Sequence 142799, A
17	586	93.0	540	22	US-09-792-2008-18	Sequence 18, App1
18	586	93.0	540	22	US-09-792-2008-18	Sequence 18, App1
19	553	87.8	154	28	US-10-221-279-6972	Sequence 6972, App
20	515.5	81.8	368	22	US-09-760-484-477	Sequence 477, App
21	515.5	81.8	368	22	US-10-211-364-1048	Sequence 1048, App
22	515.5	81.8	368	28	US-10-216-893-296	Sequence 296, App
23	515.5	81.8	368	28	US-10-217-651-431	Sequence 431, App
24	404.5	64.2	518	22	US-09-791-537-19102	Sequence 19102, A
25	404.5	64.2	524	22	US-09-791-537-88445	Sequence 88445, A
26	404.5	64.2	623	32	US-60-453-050-13203	Sequence 13203, A
27	404.5	64.2	623	32	US-60-453-135-13203	Sequence 13203, A
28	404.5	64.2	623	32	US-60-466-412-13203	Sequence 13203, A
29	404.5	64.2	664	22	US-09-791-537-107561	Sequence 107561, A
30	404.5	64.2	769	22	US-09-791-537-137085	Sequence 137085, A
31	404.5	64.2	769	24	US-09-949-016-9605	Sequence 9605, App
32	404.5	64.2	769	24	US-09-949-016-9606	Sequence 9606, App
33	404.5	64.2	769	32	US-60-453-050-13202	Sequence 13202, A
34	404.5	64.2	769	32	US-60-453-135-13202	Sequence 13202, A
35	404.5	64.2	769	32	US-60-466-412-13202	Sequence 13202, A
36	404.5	64.2	773	22	US-09-791-537-137203	Sequence 137203, A
37	404.5	64.2	775	32	US-60-453-050-13204	Sequence 13204, A
38	404.5	64.2	775	32	US-60-453-135-13204	Sequence 13204, A
39	404.5	64.2	775	32	US-60-466-412-13204	Sequence 13204, A
40	404.5	64.2	785	32	US-60-212-656-502	Sequence 502, App
41	404.5	64.2	785	32	US-60-230-435-1310	Sequence 1310, App
42	404.5	64.2	808	32	US-60-207-315-350	Sequence 350, App
43	404.5	64.2	858	32	US-60-212-656-480	Sequence 480, App
44	404.5	64.2	858	32	US-60-230-435-1465	Sequence 1465, App
45	376.5	59.8	664	32	US-60-230-435-1070	Sequence 1070, App

ALIGNMENTS

RESULT 1
US-09-949-016-11203
Sequence 11203, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11203
LENGTH: 686
TYPE: PRT
ORGANISM: Human
US-09-949-016-11203

```
Query Match          100.0%; Score 630; DB 24; Length 686;
Best Local Similarity 100.0%; Pred. No. 6.6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60
    |||||
DB 350 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 409
    |||||

QY 61 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 104
    |||||
DB 410 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 453
    |||||

RESULT 2
US-09-631-534-2
; Sequence 2, Application US/09631534
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Tafel, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/09/631,534
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-534-2

Query Match          100.0%; Score 630; DB 20; Length 696;
Best Local Similarity 100.0%; Pred. No. 6.6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60
    |||||
DB 373 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 432
    |||||

QY 61 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 104
    |||||
DB 433 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 476
    |||||

RESULT 3
US-09-809-617-2
; Sequence 2, Application US/09809617
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-09-809-617-2

Query Match          100.0%; Score 630; DB 23; Length 696;
Best Local Similarity 100.0%; Pred. No. 6.6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60
    |||||
DB 373 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 432
    |||||

QY 61 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 104
    |||||
DB 433 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 476
    |||||

RESULT 4
US-09-809-790-2
; Sequence 2, Application US/09809790
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-790-2

Query Match          100.0%; Score 630; DB 23; Length 696;
Best Local Similarity 100.0%; Pred. No. 6.6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60
    |||||
DB 373 PTKLEPTECGNGYVAGEECDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 432
    |||||

QY 61 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 104
    |||||
DB 433 RGYECRDVAVNECDITEYCTGDSGQCPNLAHKODGYACNONOGRG 476
    |||||

RESULT 5
US-10-260-506-2
; Sequence 2, Application US/10260506
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Tafel, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/10/260,506
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
```


TYPE: PRT
ORGANISM: Homo sapiens
US-10-260-506-2

Query Match
Best Local Similarity 100.0%; Score 630; DB 28; Length 696;
Pred. No. 6,6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHCSDPCCNNTSCLFOP 60
DB 373 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHCSDPCCNNTSCLFOP 432

QY 61 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 104
DB 433 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 475

RESULT 6

US-09-631-534-10
Sequence 10, Application US/09631534

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
FILE REFERENCE: 98-28C1
CURRENT APPLICATION NUMBER: US/09/631,534
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/092,371
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/147, 410
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-534-10

Query Match
Best Local Similarity 100.0%; Score 630; DB 20; Length 709;
Pred. No. 6,7e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHSDGPPCCNNTSCLFOP 60
DB 373 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHSDGPPCCNNTSCLFOP 432

QY 61 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 104
DB 433 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 476

RESULT 7

US-10-260-506-10
Sequence 10, Application US/10260506

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
FILE REFERENCE: 98-29C1
CURRENT APPLICATION NUMBER: US/10/260,506
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/092,371
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/147, 410

PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
US-10-260-506-10

Query Match
Best Local Similarity 100.0%; Score 630; DB 28; Length 709;
Pred. No. 6,7e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHCSDPCCNNTSCLFOP 60
DB 373 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHCSDPCCNNTSCLFOP 432

QY 61 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 104
DB 433 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 476

RESULT 8
US-09-760-484-315
Sequence 315, Application US/09760484

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT243
CURRENT APPLICATION NUMBER: US/09/760,484
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 315
LENGTH: 776
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (731)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-484-315

Query Match
Best Local Similarity 100.0%; Score 630; DB 22; Length 776;
Pred. No. 7,2e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHCSDPCCNNTSCLFOP 60
DB 440 PTKLFEPTGCGNGVGEAGEECDCGFHVECYGLCKCKKSLNSGAHCSDPCCNNTSCLFOP 499

QY 61 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 104
DB 500 RGYECRDVAVNECDITTEYCTGDSGCCPPNLHKODGYACNONOGRG 543

RESULT 9

US-09-634-252A-4
Sequence 4, Application US/09634252A

GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: SVP3-15 AND SVP3-17 DNA AND POLYPEPTIDES
FILE REFERENCE: 03260,0051-00304
CURRENT APPLICATION NUMBER: US/09/634,252A
CURRENT FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/074,310
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4

LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-09-634-252A-4

Query Match 100.0%; Score 630; DB 20; Length 832;
Best Local Similarity 100.0%; Pred. No. 7.6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFEPTCEGNGYVEAGEBCDGFHVECYGLCKKCSLSNGAHCSDBGPCNNITSCLP 60
Db 496 PTKLFEPTCEGNGYVEAGEBCDGFHVECYGLCKKCSLSNGAHCSDBGPCNNITSCLP 555

QY 61 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 104
Db 556 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 599

RESULT 10
US-09-791-537-64795
Sequence 64795, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patent version 3.0
SEQ ID NO 64795
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-64795

Query Match 100.0%; Score 630; DB 22; Length 832;
Best Local Similarity 100.0%; Pred. No. 7.6e-46;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFEPTCEGNGYVEAGEBCDGFHVECYGLCKKCSLSNGAHCSDBGPCNNITSCLP 60
Db 496 PTKLFEPTCEGNGYVEAGEBCDGFHVECYGLCKKCSLSNGAHCSDBGPCNNITSCLP 555

QY 61 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 104
Db 556 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 599

Search completed: October 21, 2003, 10:20:42
Job time : 316.616 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:08:40 ; Search time 9.33962 Seconds
(without alignments)
190.928 Million cell updates/sec

Title: US-09-634-252A-4_COPY_532_586
Perfect score: 332
Sequence: 1 CSLSNGAHCSGDPCCNNTSC.....CDITEYCTGSGQCPNHLK 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 153893 seqs, 32421815 residues

Total number of hits satisfying chosen parameters: 153893

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
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5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	100.0	832	7	US-60-495-114-1465 Sequence 1465, Ap
2	332	100.0	832	7	US-60-495-114-1466 Sequence 1466, Ap
3	213	64.2	369	7	US-60-495-114-1961 Sequence 1961, Ap
4	213	64.2	623	7	US-60-487-610-2161 Sequence 2161, Ap
5	213	64.2	623	7	US-60-485-450-1482 Sequence 1482, Ap
6	213	64.2	623	7	US-60-495-114-1962 Sequence 1962, Ap
7	213	64.2	769	7	US-60-487-610-2160 Sequence 2160, Ap
8	213	64.2	769	7	US-60-485-450-1481 Sequence 1481, Ap
9	213	64.2	769	7	US-60-495-114-1963 Sequence 1963, Ap
10	213	64.2	773	7	US-60-495-114-1964 Sequence 1964, Ap
11	213	64.2	775	7	US-60-487-610-2162 Sequence 2162, Ap
12	213	64.2	775	7	US-60-485-450-1483 Sequence 1483, Ap
13	185	55.7	761	7	US-60-495-114-1301 Sequence 1301, Ap
14	185	55.7	761	7	US-60-495-114-1302 Sequence 1302, Ap
15	185	55.7	823	7	US-60-490-890-1043 Sequence 1043, Ap
16	185	55.7	823	7	US-60-495-114-1304 Sequence 1304, Ap
17	185	55.7	823	7	US-60-495-114-1309 Sequence 1309, Ap
18	185	55.7	853	7	US-60-495-114-1310 Sequence 1310, Ap
19	185	55.7	859	7	US-60-490-890-1039 Sequence 1039, Ap
20	185	55.7	864	7	US-60-495-114-1308 Sequence 1308, Ap
21	185	55.7	870	7	US-60-490-890-1041 Sequence 1041, Ap
22	185	55.7	870	7	US-60-495-114-1305 Sequence 1305, Ap
23	185	55.7	870	7	US-60-495-114-1311 Sequence 1311, Ap
24	185	55.7	893	7	US-60-495-114-1307 Sequence 1307, Ap
25	185	55.7	899	7	US-60-495-114-1303 Sequence 1303, Ap
26	185	55.7	899	7	US-60-495-114-1306 Sequence 1306, Ap

27	185	55.7	900	7	US-60-495-114-1312 Sequence 1312, Ap
28	168.5	50.8	336	7	US-60-495-114-1584 Sequence 1584, Ap
29	168.5	50.8	398	1	PCT-US03-26780-1448 Sequence 1448, Ap
30	168.5	50.8	409	7	US-60-495-114-1583 Sequence 1583, Ap
31	168.5	50.8	652	7	US-60-495-114-1585 Sequence 1585, Ap
32	168.5	50.8	778	7	US-60-487-610-1926 Sequence 1926, Ap
33	168.5	50.8	781	7	US-60-487-610-1924 Sequence 1924, Ap
34	168.5	50.8	802	7	US-60-487-610-1925 Sequence 1925, Ap
35	168.5	50.8	814	1	PCT-US03-28751-4 Sequence 4, Appl
36	168.5	50.8	814	7	US-60-490-890-1713 Sequence 1713, Ap
37	167	50.3	499	6	US-10-664-456-6 Sequence 6, Appl
38	167	50.3	781	6	US-10-664-456-16 Sequence 16, Appl
39	167	50.3	790	6	US-10-664-456-15 Sequence 15, Appl
40	167	50.3	790	6	US-10-156-028A-2 Sequence 2, Appl
41	167	50.3	790	7	US-60-495-114-1565 Sequence 1565, Ap
42	160	48.2	391	1	PCT-US03-30720-2211 Sequence 2211, Ap
43	160	48.2	391	1	PCT-US03-30720-2490 Sequence 2490, Ap
44	160	48.2	746	6	US-10-670-184-4 Sequence 4, Appl
45	160	48.2	787	1	PCT-US03-30720-951 Sequence 951, Ap

ALIGNMENTS

RESULT 1
US-60-495-114-1465
Sequence 1465, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
FILE REFERENCE: CLO01480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1465
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1465

Query Match 100.0%; Score 332; DB 7; Length 832;
Best Local Similarity 100.0%; Pred. No. 5.5e-16;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSLSNGAHCSGDPCCNNTSCLFQPRGYECRAVNECDITEYCTGDSGQCPNHLK 55
|||||
Db 532 CSLSNGAHCSGDPCCNNTSCLFQPRGYECRAVNECDITEYCTGDSGQCPNHLK 586

RESULT 2
US-60-495-114-1466
Sequence 1466, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
FILE REFERENCE: CLO01480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1466
LENGTH: 832
TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1466

Query Match 100.0%; Score 332; DB 7; Length 832;
Best Local Similarity 100.0%; Pred. No. 5.5e-16;

[illegible]

RESULT 3
US-60-495-114-1961

```

: Sequence 1961, Application US/60495114
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
: TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL001480
: CURRENT APPLICATION NUMBER: US/60/495,114
: CURRENT FILING DATE: 2003-08-15
: NUMBER OF SEQ ID NOS: 91238
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1961
: LENGTH: 369
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-495-114-1961

```

	Query March	64.2%	Score 213	DB 7	Length 369
	Best Local Similarity	65.5%	Pred. No. 3	le-08	
	Matches . 36;	Conservative	6;	Mismatches 11,	Indels 2; Gaps 1
OY	1	CSLSNGAHCSGPPCCNNNTSCLEFQPGFYGCRAVNECDITETVTSGSGCQCPPLMLK	55		
		:::::	:::::		
Db	223	CTLTHDAWCSJOLCCR--CKYEPFGVSACREVNVCDDIAETGTSSQCQPPMLAK	275		

RESULT 4
US-60-487-610-2361

```

: Sequence 2361, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2361
: LENGTH: 623
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-60-487-610-2361

```

Query March	64.2%	Score 213	DB 7	Length 623
Best Local Similarity	65.5%	Pred. No. 4.7e-08		
Matches 36	Conservative 6	Mismatches 11	Indels 2	Gaps 1

Oy	1	CSLSNGAHCSPCCNNTSCLEFQPGYEGCRDVAEMCDITEYGTGSGCCPNLAK	55
		:::::	
Db	477	CTLTHDAMCSGLCCRR--CKKEPGVASCREVAEMCDIAETGTGSSGCCPNLAK	529

RESULT 5
US-60-485-450-1482

```

: Sequence 1482, Application US/60485450
:
: GENERAL INFORMATION:
:
: APPLICANT: CARGILL, Michele
:
: APPLICANT: CHANG, Sheng-Yung
:
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
:
: TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
:
: TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES

```

```

; TITLE OF INVENTION: THEREOF
;
; FILE REFERENCE: C0001470
;
; CURRENT APPLICATION NUMBER: US/60/485,450
;
; CURRENT FILING DATE: 2003-07-09
;
; NUMBER OF SEQ ID NOS: 47859
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 1482
;
; LENGTH: 623
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
US-60-485-450-1482

```

Query Match	64.2%	Score 213	DB 7	length 623
Best Local Similarity	65.5%	Pred. No.	4.7e-08	
Matches 36	Conservative 6	Mismatches 11	Indels 2	Gaps 1

```
OY      1 CSLSNGAHCSDDGPCNNNTSLFQPRGYECRDVAVECDITYCTGSGQCPLNLHK 55  
          |||::|||::|||::|||::|||::|||::|||  
DB     -477 CTLTHDAMCSDGLCCRR--CKYPEPVGSCREAVNECDIAETCTGGSSQCPLNLHK 529
```

RESULT 6
US-60-495-114-1962

```

: Sequence 1962, Application US/60495114
:
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
: TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CLO01480
: CURRENT APPLICATION NUMBER: US/60/495,114
: CURRENT FILING DATE: 2003-08-15
: NUMBER OF SEQ ID NOS: 91238
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1962
: LENGTH: 623
: TYPE: PR1
: ORGANISM: Homo sapiens
: US-60-495-114-1962

```

Query Match 64.2%; Score 213; DB 7; Length 623;
Best Local Similarity 65.5%; Pred. No. 4.7E-08;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1

OY 1 CSLSNGAHCSPCCNNTSCLFQRYGECRAVAVNECDTETCTGDSGCCPNNLR 55
 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 477 CTLIHDWMCSSGLCCRR--CKYERGVSRCRAVNEDCIATCTGDSSGCCPNLNR 529

RESULT 7
US-60-487-610-2360

```

: Sequence 2360, Application US/60487610
:
: GENERAL INFORMATION:
:
: APPLICANT: CARGILL, Michele
:
: APPLICANT: HUANG, Honglin
:
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
:
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
:
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CL001469
:
: CURRENT APPLICATION NUMBER: US/60/487,610
:
: CURRENT FILING DATE: 2003-07-17
:
: NUMBER OF SEQ ID NOS: 97101
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 2360
:
: LENGTH: 769
:
: TYPE: PR1
:
: ORGANISM: Homo sapiens
:
: US-60-487-610-2360

```

Query Match	64.2%	Score 213	DB 7	Length 769
Best Local Similarity	65.5%	Pred. No.	5.5e-08	
Matches 36	Conservative	6	Mismatches 11	Indels 2
				Gaps 1

Qy 1 CSLSNGAHCSDBGCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNHLK 55
Db 477 CTLLTHDAMCSDGLCCRR--CKYEBRGVSCREAVNECDIAETCTGDSGCCPPNHLK 529

RESULT 8
US-60-485-450-1481

; Sequence 1481, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1481
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1481

Query Match 64.2%; Score 213; DB 7; Length 763;
Best Local Similarity 65.5%; Pred. No. 5.5e-08;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSLSNGAHCSDBGCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNHLK 55
Db 477 CTLLTHDAMCSDGLCCRR--CKYEBRGVSCREAVNECDIAETCTGDSGCCPPNHLK 529

RESULT 9
US-60-495-114-1963

; Sequence 1963, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1963
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1963

Query Match 64.2%; Score 213; DB 7; Length 765;
Best Local Similarity 65.5%; Pred. No. 5.5e-08;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSLSNGAHCSDBGCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNHLK 55
Db 477 CTLLTHDAMCSDGLCCRR--CKYEBRGVSCREAVNECDIAETCTGDSGCCPPNHLK 529

RESULT 10
US-60-495-114-1964

; Sequence 1964, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114

; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1964
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1964

Query Match 64.2%; Score 213; DB 7; Length 773;
Best Local Similarity 65.5%; Pred. No. 5.5e-08;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSLSNGAHCSDBGCCNNTSCLFQPRGYECRDVAVNECDITEYCTGDSGCCPPNHLK 55
Db 477 CTLLTHDAMCSDGLCCRR--CKYEBRGVSCREAVNECDIAETCTGDSGCCPPNHLK 529

Search completed: October 21, 2003, 10:21:22
Job time : 9.33962 secs

LOCATION: (323)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-484-477

Query Match 100.0%; Score 332; DB 22; Length 368;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSLSGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITREYCTGDSGCCPPLHK 55
DB 68 CSLSGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITREYCTGDSGCCPPLHK 122

RESULT 2
US-10-211-364-1048
Sequence 1048, Application US/10211364

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P216CIN
CURRENT APPLICATION NUMBER: US/10/211,364
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: 09/760,486
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1778
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1048
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: misc_feature
LOCATION: (33)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: misc_feature
LOCATION: (323)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-211-364-1048

Query Match 100.0%; Score 332; DB 28; Length 368;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSLSGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITREYCTGDSGCCPPLHK 55
DB 68 CSLSGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITREYCTGDSGCCPPLHK 122

RESULT 3

US-10-216-893-296
Sequence 296, Application US/10216893
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P216CIN
CURRENT APPLICATION NUMBER: US/10/216,893
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 09/760,454
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 573
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 296
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: misc_feature
LOCATION: (33)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: misc_feature
LOCATION: (323)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-216-893-296

Query Match 100.0%; Score 332; DB 28; Length 368;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSLSGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITREYCTGDSGCCPPLHK 55
DB 68 CSLSGAHCSDGPCNNNTSCLFQPRGYECRDVAVNECDITREYCTGDSGCCPPLHK 122

RESULT 4
US-10-217-651-431

Sequence 431, Application US/10217651
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P216CIN
CURRENT APPLICATION NUMBER: US/10/217,651
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 09/760,491
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886
 PRIOR FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: 60/217,487
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 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/217,496
 PRIOR FILING DATE: 2000-07-11
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 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/218,290
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/225,757
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/226,868
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: 60/216,647
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/225,267
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/216,880
 PRIOR FILING DATE: 2000-07-07
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 PRIOR APPLICATION NUMBER: 60/251,869
 PRIOR FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: 60/235,834
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: 60/234,274
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 PRIOR APPLICATION NUMBER: 60/234,223
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 PRIOR APPLICATION NUMBER: 60/224,518
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/236,369
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/224,519
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/220,964
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/241,809
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/249,299
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/236,327
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/241,785
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/244,617
 PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: 60/225,268
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/236,368
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/251,856
 PRIOR FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: 60/251,868
 PRIOR FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: 60/229,344
 PRIOR FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: 60/229,345
 PRIOR FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: 60/229,287
 PRIOR FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: 60/229,513

PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/231,413
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/229,509
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/236,367
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/237,039
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/237,038
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/236,370
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: 60/236,802
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/237,037
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/237,040
 PRIOR FILING DATE: 2000-10-02
 PRIOR APPLICATION NUMBER: 60/240,960
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/239,935
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: 60/239,937
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: 60/241,787
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/246,474
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/246,532
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/249,216
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 PRIOR FILING DATE: 2000-08-22
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 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/235,836
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: 60/230,438
 PRIOR FILING DATE: 2000-09-06
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 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: 60/225,266
 PRIOR FILING DATE: 2000-08-14
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 PRIOR APPLICATION NUMBER: 60/249,212
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,207
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,245
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,244
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,217
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,211
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,215

OTHER INFORMATION: Fusion Construct
US-09-792-200B-18

Query Match 100.0%; Score 332; DB 22; Length 540;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CSLSNGAHCSGDPCCNNTSCIFQPRGYECRDVAVNECDITTEYCTGDSGQCPNHLK 55
68 CSLSNGAHCSGDPCCNNTSCIFQPRGYECRDVAVNECDITTEYCTGDSGQCPNHLK 122

RESULT 5
US-09-792-200B-18

Sequence 18, Application US/09792200B

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Fanslow, William C.

APPLICANT: Poindexter, Kurt M.

APPLICANT: Cerretti, Douglas P.

APPLICANT: Black, Roy A.

TITLE OF INVENTION: INTEGRIN ANTAGONISTS

FILE REFERENCE: 2958-A

CURRENT APPLICATION NUMBER: US/09/792,200B

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: US 60/184,865

PRIOR FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 18

LENGTH: 540

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion Construct
US-09-792-200C-18

Query Match 100.0%; Score 332; DB 22; Length 540;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CSLSNGAHCSGDPCCNNTSCIFQPRGYECRDVAVNECDITTEYCTGDSGQCPNHLK 55
50 CSLSNGAHCSGDPCCNNTSCIFQPRGYECRDVAVNECDITTEYCTGDSGQCPNHLK 104

RESULT 6
US-09-792-200C-18

Sequence 18, Application US/09792200C

GENERAL INFORMATION:

APPLICANT: Fanslow III, William C.

APPLICANT: Poindexter, Kurt M.

APPLICANT: Cerretti, Douglas P.

APPLICANT: Black, Roy A.

TITLE OF INVENTION: INTEGRIN ANTAGONISTS

FILE REFERENCE: 2958-A

CURRENT APPLICATION NUMBER: US/09/792,200C

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: US 60/184,865

PRIOR FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 18

LENGTH: 540

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion Construct
US-09-792-200C-18

Query Match 100.0%; Score 332; DB 22; Length 540;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CSLSNGAHCSGDPCCNNTSCIFQPRGYECRDVAVNECDITTEYCTGDSGQCPNHLK 55
50 CSLSNGAHCSGDPCCNNTSCIFQPRGYECRDVAVNECDITTEYCTGDSGQCPNHLK 104

RESULT 7
US-09-949-016-11203

Sequence 11203, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11203

LENGTH: 686

TYPE: PRT

ORGANISM: Human

US-09-949-016-11203

Query Match 100.0%; Score 332; DB 24; Length 686;
Best Local Similarity 100.0%; Pred. No. 8.4e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 386 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 440

RESULT 8

US-09-631-534-2
 ; Sequence 2, Application US/09631534
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Baindur, Nand
 ; APPLICANT: Deisher, Theresa A.
 ; APPLICANT: Bishop, Paul D.
 ; APPLICANT: Talt, David W.
 ; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
 ; FILE REFERENCE: 98-29C1
 ; CURRENT APPLICATION NUMBER: US/09/631,534
 ; CURRENT FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 60/092,371
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/147, 410
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 09/351,414
 ; PRIOR FILING DATE: 1999-07-09
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 696
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-631-534-2

Query Match 100.0%; Score 332; DB 20; Length 696;
 Best Local Similarity 100.0%; Pred. No. 8.5e-25;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 55
 Db 409 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 463

RESULT 9

US-09-809-617-2
 ; Sequence 2, Application US/09809617
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Baindur, Nand
 ; APPLICANT: Deisher, Theresa A.
 ; APPLICANT: Bishop, Paul D.
 ; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
 ; FILE REFERENCE: 98-29
 ; CURRENT APPLICATION NUMBER: US/09/809,617
 ; CURRENT FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: US/09/351,414
 ; PRIOR FILING DATE: 1999-07-09
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 696
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-809-617-2

Query Match 100.0%; Score 332; DB 23; Length 596;
 Best Local Similarity 100.0%; Pred. No. 8.5e-25;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 55
 Db 409 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 463

RESULT 10

US-09-809-790-2
 ; Sequence 2, Application US/09809790
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Baindur, Nand
 ; APPLICANT: Deisher, Theresa A.
 ; APPLICANT: Bishop, Paul D.
 ; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
 ; FILE REFERENCE: 98-29
 ; CURRENT APPLICATION NUMBER: US/09/809,790
 ; CURRENT FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 09/351,414
 ; PRIOR FILING DATE: 1999-07-09
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 696
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-809-790-2

Query Match 100.0%; Score 332; DB 23; Length 696;
 Best Local Similarity 100.0%; Pred. No. 8.5e-25;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 55
 Db 409 CSLSNGAHCSDGPCNNNTSCLFQPRGYECRDAVNECDITTEYCTGDSGQCPNHLK 463

Search completed: October 21, 2003, 10:20:42
 Job time : 166.384 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:27:07 ; Search time 1871.38 Seconds

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	332	100.0	1668	33	US-09-792-200C-17	Sequence 17, Appl
3	332	100.0	2268	27	US-09-631-534-1	Sequence 1, Appl
4	332	100.0	2268	34	US-09-809-617-1	Sequence 1, Appl
5	332	100.0	2268	34	US-09-809-790-1	Sequence 1, Appl
6	332	100.0	2268	49	US-10-260-506-1	Sequence 1, Appl
7	332	100.0	2294	40	US-09-949-016-5332	Sequence 5332, Ap
8	332	100.0	2499	27	US-09-634-252A-2	Sequence 2, Appl
9	332	100.0	2499	48	US-10-202-675-2	Sequence 2, Appl
10	332	100.0	2899	21	US-10-170-235-22436	Sequence 22436, A
11	332	100.0	2899	21	US-09-496-321-82	Sequence 82, Appl
12	332	100.0	2899	21	US-09-496-321-109	Sequence 109, Appl
13	332	100.0	2859	65	US-60-118-905-82	Sequence 82, Appl
14	332	100.0	2859	65	US-60-118-905-109	Sequence 109, Appl
15	332	100.0	3054	46	US-10-126-052A-149	Sequence 149, Appl
16	332	100.0	3054	46	US-10-126-052A-324	Sequence 324, Appl
17	332	100.0	3402	33	US-09-760-484-177	Sequence 177, Appl
18	332	100.0	3402	48	US-10-211-364-395	Sequence 395, Appl
19	332	100.0	3402	48	US-10-211-893-114	Sequence 114, Appl
20	332	100.0	3402	48	US-10-211-651-164	Sequence 164, Appl
21	332	100.0	4043	51	US-09-824-129-2	Sequence 2, Appl
22	332	100.0	4440	33	US-09-359-464-2	Sequence 15, Appl
23	332	100.0	4440	33	US-09-760-484-15	Sequence 9, Appl
24	332	100.0	4720	27	US-10-260-506-9	Sequence 9, Appl
25	332	100.0	4720	49	US-10-260-506-9	Sequence 9, Appl
26	332	100.0	6391	71	US-60-172-360-21719	Sequence 21719, A
27	332	100.0	6400	42	US-09-976-594-61	Sequence 61, Appl
28	332	100.0	6400	79	US-60-240-409-61	Sequence 61, Appl
29	332	100.0	6400	87	US-60-324-185-1573	Sequence 1573, Ap
30	325	97.9	494	17	US-09-234-611-16347	Sequence 16347, A
31	325	97.9	494	17	US-09-235-076-22101	Sequence 22101, A
32	325	97.9	494	18	US-09-289-768-20173	Sequence 20173, A
33	325	97.9	494	19	US-09-332-782-22101	Sequence 22101, A
34	325	97.9	494	32	US-09-737-223-22101	Sequence 22101, A
35	325	97.9	494	38	US-09-904-809-16347	Sequence 16347, A
36	325	97.9	494	38	US-09-918-985-22101	Sequence 22101, A
37	325	97.9	494	39	US-09-935-337-20173	Sequence 20173, A
38	319	96.1	2271	46	US-10-144-771-15737	Sequence 15737, A
39	319	96.1	2271	91	US-60-360-207-15737	Sequence 15737, A
40	319	96.1	6401	75	US-60-213-359-127	Sequence 127, App
41	315	94.9	468	22	US-09-519-705-803	Sequence 803, App
42	315	94.9	468	25	US-09-574-454-803	Sequence 803, App
43	315	94.9	468	48	US-10-221-279-792	Sequence 792, Appl
44	308	92.8	261	7	US-08-275-627-52	Sequence 52, Appl
45	308	92.8	261	7	US-08-275-627A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-792-200B-17
Sequence 17, Application US/09792200B
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Fanslow, William C.
APPLICANT: Poindexter, Kurt
APPLICANT: Cerretti, Douglas P.
APPLICANT: Black, Roy A.
TITLE OF INVENTION: INTEGRIN ANTAGONISTS
FILE REFERENCE: 2958-A
CURRENT APPLICATION NUMBER: US/09/792,200B
CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: US 60/184,865
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1668
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion Construct
NAME/KEY: CDS
LOCATION: (25)..(1647)
OTHER INFORMATION:
US-09-792-200B-17

Alignment Scores:

Pred. No.: 2,666-28
Score: 332.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 33
Length: 1668
Matches: 55
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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QY 1 CysSerLeuSerAengLYAlAHicYSerSerhspGlyProCYsCYsAsnAsnThsSerCYs 20

DB 172 TGTTCCTCTCAACGGGGCTCAGTCAGCGACGGGCCCTCTGTAAACATACCTCATGT 231

QY 21 LeupheginProArgGlyTYrGluCYsArgAspAlaValaAngluCYsAspIleThrlu 40

DB 222 CTTTTCAGCCACGACGGGATGAAATGCCGGGATGCTGGAACGAGTGTATTAATGAA 291

QY 41 TyrCYsThrGlyAspSerGlyGluCYsProProAsnLeuHISlys 55

DB 292 TATTTACTGGAGACTCTGTGTCAGTCCACCAATCTTCTTAAG 336

RESULT 2

US-09-792-200C-17
Sequence 17, Application US/09792200C

GENERAL INFORMATION:
APPLICANT: Fanslow, III, William C.
APPLICANT: Poindexter, Kurt M.
APPLICANT: Cerretti, Douglas P.
APPLICANT: Black, Roy A.
TITLE OF INVENTION: INTEGRIN ANTAGONISTS
FILE REFERENCE: 2958-A
CURRENT APPLICATION NUMBER: US/09/792,200C
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/184,865
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 1668
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion Construct
NAME/KEY: CDS
LOCATION: (25)..(1647)
OTHER INFORMATION:
US-09-792-200C-17

Alignment Scores:

Pred. No.: 2,666-28
Score: 332.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 33
Length: 1668
Matches: 55
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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US-09-634-252a-4_COPY_532_586 (1-55) x US-09-792-200C-17 (1-1668)
Qy 1 CySerleuseranglialahisCySerAspGlyProCyCySaenAntThSerCys 20
Db 172 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTGTAACAATACCTCATGT 231
Qy 21 LeuPheGlnProArgGlyTyrgluCyArgAspAlaValansgluCyAspIleThrglu 40
Db 232 CTTTTCAGCCACGAGGATGTAATGCGGGATGCTGTGAACGAGTGTGATTACTGAA 291
Qy 41 TyrCyThrGlyAspSerGlyGlnCyProProAsnleuHislys 55
Db 292 TATTGTACTGAGACTCTGTGTGATGCGCCACCAATCTTCATAAG 336

RESULT 3
US-09-631-534-1
; Sequence 1, Application US/09631534
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Baidur, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Telft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/09/631,534
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2090)
; NAME/KEY: misc_feature
; LOCATION: (1)...(2268)
; OTHER INFORMATION: n = A,T,C or G
US-09-631-534-1

Alignment Scores:
Pred. No.: 3,79e-28 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-631-534-1 (1-2268)
Qy 1 CySerleuseranglialahisCySerAspGlyProCyCySaenAntThSerCys 20
Db 1227 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTGTAACAATACCTCATGT 1286
Qy 21 LeuPheGlnProArgGlyTyrgluCyArgAspAlaValansgluCyAspIleThrglu 40
Db 1287 CTTTTCAGCCACGAGGATGTAATGCGGGATGCTGTGAACGAGTGTGATTACTGAA 1346
Qy 41 TyrCyThrGlyAspSerGlyGlnCyProProAsnleuHislys 55
Db 1347 TATTGTACTGAGACTCTGTGTGATGCGCCACCAATCTTCATAAG 1391

RESULT 4
US-09-809-617-1
; Sequence 1, Application US/09809617
; GENERAL INFORMATION:
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APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Baidur, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/809,617
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US/09/351,414
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-809-790-1

Alignment Scores:
Pred. No.: 3,79e-28 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 34 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-809-617-1 (1-2268)
Qy 1 CySerleuseranglialahisCySerAspGlyProCyCySaenAntThSerCys 20
Db 1227 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTGTAACAATACCTCATGT 1286
Qy 21 LeuPheGlnProArgGlyTyrgluCyArgAspAlaValansgluCyAspIleThrglu 40
Db 1287 CTTTTCAGCCACGAGGATGTAATGCGGGATGCTGTGAACGAGTGTGATTACTGAA 1346
Qy 41 TyrCyThrGlyAspSerGlyGlnCyProProAsnleuHislys 55
Db 1347 TATTGTACTGAGACTCTGTGTGATGCGCCACCAATCTTCATAAG 1391

RESULT 5
US-09-809-790-1
; Sequence 1, Application US/09809790
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Baidur, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2090)
; NAME/KEY: misc_feature
; LOCATION: (1)...(2268)
; OTHER INFORMATION: n = A,T,C or G
US-09-809-790-1
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Alignment Scores:

Pred. No.: 3,798-28 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 34 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-809-790-1 (1-2268)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20

DB 1227 TGTTCCTCTCCACAGGGGCTCAGTCAGCGAGCGGGCCCTGCTGTAACTCTCATGT 1286

QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

DB 1287 CTTTTCAGCCAGAGGGATGAATGCCGGATGCTGTGAACGAGTGTGATTACTGAA 1346

QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

DB 1347 TATTGTACTGAGACTCTGTGTCAGTCCACCAATCTTCATTAAG 1391

RESULT 6

US-10-260-506-1

; Sequence 1, Application US/10260506

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Baird, Nand

; APPLICANT: Deisher, Theresa A.

; APPLICANT: Bishop, Paul D.

; APPLICANT: Taft, David W.

; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP

; FILE REFERENCE: 98-29CI

; CURRENT APPLICATION NUMBER: US/10/260,506

; CURRENT FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: 60/092,371

; PRIOR FILING DATE: 1998-07-10

; PRIOR APPLICATION NUMBER: 60/147, 410

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 09/351,414

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2268

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3)...(2090)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(2268)

; OTHER INFORMATION: n = A,T,C or G

US-10-260-506-1

Alignment Scores:

Pred. No.: 3,798-28 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 49 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-10-260-506-1 (1-2268)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20

DB 1227 TGTTCCTCTCCACAGGGGCTCAGTCAGCGAGCGGGCCCTGCTGTAACTCTCATGT 1286

QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

DB 1287 CTTTTCAGCCAGAGGGATGAATGCCGGATGCTGTAACGAGTGTGATTACTGAA 1346

QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

DB 1347 TATTGTACTGAGACTCTGTGTCAGTCCACCAATCTTCATTAAG 1391

RESULT 7

US-09-949-016-5332

; Sequence 5332, Application US/09949016

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5332

; LENGTH: 2394

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-5332

Alignment Scores:

Pred. No.: 4,046-28 Length: 2394
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-949-016-5332 (1-2394)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20

DB 1158 TGTTCCTCTCCACAGGGGCTCAGTCAGCGAGCGGGCCCTGCTGTAACTCTCATGT 1217

QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

DB 1218 CTTTTCAGCCAGAGGGATGAATGCCGGATGCTGTGAACGAGTGTGATTACTGAA 1277

QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

DB 1278 TATTGTACTGAGACTCTGTGTCAGTCCACCAATCTTCATTAAG 1322

RESULT 8

US-09-634-252a-2

; Sequence 2, Application US/09634252A

; GENERAL INFORMATION:

; APPLICANT: Cerretti, Douglas P.

; TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES

; FILE REFERENCE: 03260, 0051-00304

; CURRENT APPLICATION NUMBER: US/09/634, 252A

; CURRENT FILING DATE: 2000-08-07

; PRIOR APPLICATION NUMBER: 60/074, 310

; PRIOR FILING DATE: 1998-02-11

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 2499

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-634-252a-2

Alignment Scores:

Pred. No.: 4,246-28 Length: 2499

Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-634-252A-4_COPY_532_586 (1-55) x US-09-634-252A-2 (1-2499)

QY 1 CysSerLeuSerAenGlyAlaHisCysSerAaspGlyProCysCysAaenAntHrSerCys 20
Db 1594 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTTAACAATACCTCATGT 1653
QY 21 LeuPheGlnProAArgGlyTyrgluCysArgAaspAlaValaengluCysAaspIleThrGlu 40
Db 1654 CTTTTCAGCCACAGAGGTATGAATGCCGGGATGCTGTAACGAGTGTGATATTACTGAA 1713

QY 41 TyrcyethrGlyAaspSerGlyGlnCysProProAenLeuHisIlys 55
Db 1714 TATTGTAAGTGAAGCTGTGTCAGTCCACCAATCTTCATAAG 1758

RESULT 9

US-10-202-675-2
; Sequence 2, Application US/10202675
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: SVP3-13 AND SVP3-17 DNA AND POLYPEPTIDES
; FILE REFERENCE: 03260.0051-00304
; CURRENT APPLICATION NUMBER: US/10/202,675
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/09/634,252
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/074,310
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-202-675-2

Alignment Scores:
Pred. No.: 4,24e-28 Length: 2499
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 48 Gaps: 0

US-09-634-252A-4_COPY_532_586 (1-55) x US-10-202-675-2 (1-2499)

QY 1 CysSerLeuSerAenGlyAlaHisCysSerAaspGlyProCysCysAaenAntHrSerCys 20
Db 1594 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTTAACAATACCTCATGT 1653

QY 21 LeuPheGlnProAArgGlyTyrgluCysArgAaspAlaValaengluCysAaspIleThrGlu 40
Db 1654 CTTTTCAGCCACAGAGGTATGAATGCCGGGATGCTGTAACGAGTGTGATATTACTGAA 1713

QY 41 TyrcyethrGlyAaspSerGlyGlnCysProProAenLeuHisIlys 55
Db 1714 TATTGTAAGTGAAGCTGTGTCAGTCCACCAATCTTCATAAG 1758

RESULT 10

US-10-170-235-22436
; Sequence 22436, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: C0001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17

; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 22436
; LENGTH: 2899
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-22436

Alignment Scores:
Pred. No.: 5.03e-28 Length: 2899
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 47 Gaps: 0

US-09-634-252A-4_COPY_532_586 (1-55) x US-10-170-235-22436 (1-2899)

QY 1 CysSerLeuSerAenGlyAlaHisCysSerAaspGlyProCysCysAaenAntHrSerCys 20
Db 1663 TGTTCCTCTCCAAAGGGGCTCACTGACGACGAGGGCCCTGCTTAACAATACCTCATGT 1722

QY 21 LeuPheGlnProAArgGlyTyrgluCysArgAaspAlaValaengluCysAaspIleThrGlu 40
Db 1723 CTTTTCAGCCACAGAGGTATGAATGCCGGGATGCTGTAACGAGTGTGATATTACTGAA 1782

QY 41 TyrcyethrGlyAaspSerGlyGlnCysProProAenLeuHisIlys 55
Db 1783 TATTGTAAGTGAAGCTGTGTCAGTCCACCAATCTTCATAAG 1827

Search completed: October 21, 2003, 14:37:22
Job time: 1876.38 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 10:34:26 ; Search time 110.346 Seconds
(without alignments)
758.947 Million cell updates/sec

Title: US-09-634-252A-4_COPY_532_586
Perfect score: 332
Sequence: 1 CSLSNGAHCSDGPCNNNTSC.....CDITEYCTGDSGQCPEMLHK 55

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 6.0, Ygapext 7.0
Delop 6.0, Delext 7.0

Searched: 1640717 seqs, 76133381 residues

Total number of hits satisfying chosen parameters: 3631434

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Pending_Patents_NA_New -OFMT=fastlap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPEXT=0 -UNIT5=Dits -START=1 -END=1 -MATRIX=D10sum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=10 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELIXT=7

Database : Pending Patents_NA_New:*
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7: /cgcn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	100.0	3760	7	US-60-495-114-329
2	332	100.0	4071	7	US-60-495-114-330
3	213	64.2	1911	7	US-60-487-610-948
4	213	64.2	1911	7	US-60-485-450-577
5	213	64.2	3117	7	US-60-495-114-825
6	213	64.2	3167	7	US-60-487-610-947
7	213	64.2	3167	7	US-60-485-450-576
8	213	64.2	3185	7	US-60-487-610-949
9	213	64.2	3185	7	US-60-485-450-578
10	213	64.2	3421	7	US-60-495-114-827
11	213	64.2	3431	7	US-60-495-114-826

12	213	64.2	3433	7	US-60-495-114-828	Sequence 828, App
13	185	55.7	2636	7	US-60-490-890-1042	Sequence 1042, Ap
14	185	55.7	2744	7	US-60-490-890-1038	Sequence 1038, Ap
15	185	55.7	2775	7	US-60-495-114-168	Sequence 168, App
16	185	55.7	2775	7	US-60-495-114-173	Sequence 173, App
17	185	55.7	2865	7	US-60-495-114-174	Sequence 174, App
18	185	55.7	2876	7	US-60-495-114-166	Sequence 166, App
19	185	55.7	3347	7	US-60-490-890-1040	Sequence 1040, Ap
20	185	55.7	3759	7	US-60-495-114-172	Sequence 172, App
21	185	55.7	3777	7	US-60-495-114-169	Sequence 169, App
22	185	55.7	3777	7	US-60-495-114-175	Sequence 175, App
23	185	55.7	3801	7	US-60-495-114-171	Sequence 171, App
24	185	55.7	3819	7	US-60-495-114-167	Sequence 167, App
25	185	55.7	3819	7	US-60-495-114-170	Sequence 170, App
26	185	55.7	3867	7	US-60-495-114-176	Sequence 176, App
27	185	55.7	3878	7	US-60-495-114-165	Sequence 165, App
28	173.5	52.3	2815	1	PCT-US03-28751-6	Sequence 6, App11
29	168.5	50.8	1194	1	PCT-US03-26780-217	Sequence 217, App
30	168.5	50.8	2286	7	US-60-495-114-447	Sequence 447, App
31	168.5	50.8	2313	7	US-60-495-114-448	Sequence 448, App
32	168.5	50.8	2336	7	US-60-495-114-449	Sequence 449, App
33	168.5	50.8	2712	7	US-60-487-610-511	Sequence 511, App
34	168.5	50.8	2740	1	PCT-US03-28751-3	Sequence 3, App11
35	168.5	50.8	2740	7	US-60-490-890-1712	Sequence 1712, Ap
36	168.5	50.8	2762	7	US-60-487-610-512	Sequence 512, App
37	168.5	50.8	2808	7	US-60-487-610-513	Sequence 513, App
38	168.5	50.8	4547	7	US-60-495-114-446	Sequence 446, App
39	167	50.3	1500	6	US-10-664-456-3	Sequence 3, App11
40	167	50.3	2346	6	US-10-664-456-11	Sequence 11, App1
41	167	50.3	2373	6	US-10-664-456-10	Sequence 10, App1
42	167	50.3	2373	6	US-10-156-028A-1	Sequence 1, App11
43	167	50.3	2536	7	US-60-495-114-429	Sequence 429, App
44	167	50.3	14966	7	US-60-495-114-16886	Sequence 16886, A
45	167	50.3	50248	7	US-60-495-114-16422	Sequence 16422, A

ALIGNMENTS

RESULT 1
US-60-495-114-329
; Sequence 329, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARCILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 3760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-495-114-329
US-09-634-252A-4_COPY_532_586 (1-55) x US-60-495-114-329 (1-3760)
Alignment Scores:
Pred. No.: 2.67e-35 Length: 3760
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
QY 1 CysSerLeuSerArgGlyAlaHisCysSerAspIleProCysCysAsnAsnThrSerCys 20
DB 1817 TGTTCCTCTTCACGGGGCTCCTGACGACGCGGGCTGCTTAACATACCTCATGT 1876
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

```
Db      1877 CTTTTCACCCACGAGGTATTAATGCCGGATGCTGTGACGAGTGTGATTAATGTA 1936
Qy      41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db      1937 TATTGACTGAGACTCTGTGTGATGCCACCAAAATCTTCAATAG 1981

RESULT 2
US-60-495-114-330
; Sequence 330, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 4071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-495-114-330

Alignment Scores:
Pred. No.:      2,96e-35      Length:      4071
Score:          332.00      Matches:      55
Percent Similarity: 100.00%      Mismatches: 0
Best Local Similarity: 100.00%      Indels:      0
Query Match:    100.00%      Gaps:        0
DB:              7

US-09-634-252a-4_copy_532_586 (1-55) x US-60-495-114-330 (1-4071)

Qy      1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db      1817 TGTTCCCTCTCAGACGGGGCTCATGCGACGAGGGCCCTGTGTAACAAATACCTCATGT 1876

Qy      21 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db      1877 CTTTTCACCCACGAGGGTGTGATGCCGGATGCTGTGTAACGAGTGTGATTTACTGAA 1936

Qy      41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db      1937 TATTGACTGAGACTCTGTGTGATGCCACCAAAATCTTCAATAG 1981

RESULT 3
US-60-487-610-948
; Sequence 948, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 948
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-948

Alignment Scores:
Pred. No.:      2,93e-19      Length:      1911
Score:          213.00      Matches:      36
Percent Similarity: 76.36%      Mismatches: 6
Best Local Similarity: 65.45%      Indels:      11
Query Match:    64.16%      Gaps:        2
DB:              1

US-09-634-252a-4_copy_532_586 (1-55) x US-60-487-610-948 (1-1911)

Qy      1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db      1429 TGCACCTGACTCAGACGAGCCATGTGCGACGACGGGCTCTGTGCGCCG-----TGC 1482

Qy      21 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db      1483 AAGTACGAAACACGAGGGGTGTGCTCTGCGAGAGGCGGTGAACGAGTGGACATCGCGAG 1542

Qy      41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db      1543 ACCTCAGCGGGGACTTACGACAGTGGCCGCTTAACCTGCACAG 1587

RESULT 5
US-60-495-114-825
; Sequence 825, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 825
```

```
DB:      7      Gaps:      1

US-09-634-252a-4_copy_532_586 (1-55) x US-60-487-610-948 (1-1911)

Qy      1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db      1429 TGCACCTGACTCAGACGAGCCATGTGCGACGACGGGCTCTGTGCGCCG-----TGC 1482

Qy      21 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db      1483 AAGTACGAAACACGAGGGGTGTGCTCTGCGAGAGGCGGTGAACGAGTGGACATCGCGAG 1542

Qy      41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db      1543 ACCTCAGCGGGGACTTACGACAGTGGCCGCTTAACCTGCACAG 1587

RESULT 4
US-60-485-450-577
; Sequence 577, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 577
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-577

Alignment Scores:
Pred. No.:      2,93e-19      Length:      1911
Score:          213.00      Matches:      36
Percent Similarity: 76.36%      Mismatches: 6
Best Local Similarity: 65.45%      Indels:      11
Query Match:    64.16%      Gaps:        2
DB:              1

US-09-634-252a-4_copy_532_586 (1-55) x US-60-485-450-577 (1-1911)

Qy      1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db      1429 TGCACCTGACTCAGACGAGCCATGTGCGACGACGGGCTCTGTGCGCCG-----TGC 1482

Qy      21 LeuPheGlnProArgGlyTyrGlnCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db      1483 AAGTACGAAACACGAGGGGTGTGCTCTGCGAGAGGCGGTGAACGAGTGGACATCGCGAG 1542

Qy      41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db      1543 ACCTCAGCGGGGACTTACGACAGTGGCCGCTTAACCTGCACAG 1587
```

```
; LENGTH: 3117
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-495-114-825

Alignment Scores:
Pred. No.: 5.56e-19 Length: 3117
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 7 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x US-60-495-114-825 (1-3117)
QY 1 CysSerLeuSerAnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1115 TGCACCTGACTCAGACGCCATGTGACGACGCGGCTGTGTCGCCCGC-----TGC 1168
QY 21 LeuPheGlnProArgGlyTyrgLuCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db 1169 AAGTACGACACGCGGGGTGTCTCTGCGGAGAGCCCGTGAACGAKTGCACATCGCGGAG 1228
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
Db 1229 ACCTGACCGGGGACTCTAGCCAGTGCCTACCTGAACCTGCACAG 1273

RESULT 6
US-60-487-610-947
; Sequence 947, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487, 610
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 947
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-947

Alignment Scores:
Pred. No.: 5.68e-19 Length: 3167
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 7 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x US-60-487-610-947 (1-3167)
QY 1 CysSerLeuSerAnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1429 TGCACCTGACTCAGACGCCATGTGACGACGCGGCTGTGTCGCCCGC-----TGC 1482
QY 21 LeuPheGlnProArgGlyTyrgLuCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db 1483 AAGTACGACACGCGGGGTGTCTCTGCGGAGAGCCCGTGAACGAKTGCACATCGCGGAG 1542
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
Db 1543 ACCTGACCGGGGACTCTAGCCAGTGCCTGAACCTGCACAG 1567

RESULT 7
US-60-485-450-576
; Sequence 576, Application US/60485450
; GENERAL INFORMATION:
```

```
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 576
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-576

Alignment Scores:
Pred. No.: 5.68e-19 Length: 3167
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 7 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x US-60-485-450-576 (1-3167)
QY 1 CysSerLeuSerAnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1429 TGCACCTGACTCAGACGCCATGTGACGACGCGGCTGTGTCGCCCGC-----TGC 1482
QY 21 LeuPheGlnProArgGlyTyrgLuCysArgAspAlaValAsnGluCysAspIleThrGlu 40
Db 1483 AAGTACGACACGCGGGGTGTCTCTGCGGAGAGCCCGTGAACGAKTGCACATCGCGGAG 1542
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIys 55
Db 1543 ACCTGACCGGGGACTCTAGCCAGTGCCTGAACCTGCACAG 1587

RESULT 8
US-60-487-610-949
; Sequence 949, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487, 610
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 949
; LENGTH: 3185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-949

Alignment Scores:
Pred. No.: 5.72e-19 Length: 3185
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 7 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x US-60-487-610-949 (1-3185)
QY 1 CysSerLeuSerAnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1429 TGCACCTGACTCAGACGCCATGTGACGACGCGGCTGTGTCGCCCGC-----TGC 1482
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QY 21 LeupheginProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrglu 40
Db 1483 AAGTACGAACCGGGGGTGTCTGCTGCCAGAGCGCGTGAAGAGTGGACATCGCGAG 1542
QY 41 TyrCysThrgIyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1543 ACTGACCGGGGACTTACGACAGTCCCGCTTAACCTGCACAG 1587

RESULT 9

US-60-485-450-578
Sequence 578, Application US/60485450

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 578
LENGTH: 3185
TYPE: DNA
ORGANISM: Homo sapiens
US-60-485-450-578

Alignment Scores:

Pred. No.: 5,72e-19 Length: 3185
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 7 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x US-60-485-450-578 (1-3185)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1429 TGCACCTGACTCAGACGACCATGTGACAGCGGGCTCTGCTGCCGC-----TGC 1482
QY 21 LeupheginProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrglu 40
Db 1483 AAGTACGAACCGGGGGTGTCTGCTGCCAGAGCGCGTGAAGAGTGGACATCGCGAG 1542
QY 41 TyrCysThrgIyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1543 ACTGACCGGGGACTTACGACAGTCCCGCTTAACCTGCACAG 1587

RESULT 10

US-60-495-114-827
Sequence 827, Application US/60495114

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 827
LENGTH: 3421
TYPE: DNA
ORGANISM: Homo sapiens
US-60-495-114-827

Alignment Scores:

Pred. No.: 6,28e-19 Length: 3421
Score: 213.00 Matches: 36

Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 7 Gaps: 1

US-09-634-252a-4_COPY_532_586 (1-55) x US-60-495-114-827 (1-3421)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1429 TGCACCTGACTCAGACGACCATGTGACAGCGGGCTCTGCTGCCGC-----TGC 1482
QY 21 LeupheginProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrglu 40
Db 1483 AAGTACGAACCGGGGGTGTCTGCTGCCAGAGCGCGTGAAGAGTGGACATCGCGAG 1542
QY 41 TyrCysThrgIyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1543 ACTGACCGGGGACTTACGACAGTCCCGCTTAACCTGCACAG 1587

Search completed: October 21, 2003, 14:42:56
Job time : 115.346 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 21, 2003, 12:02:06 / Search time 140.094 Seconds
(without alignments)
1052.855 Million cell1 updates/sec

Title: US-09-634-252a-4_COPY_532_586

Perfect score: 332

Sequence: 1 CSLSNGAHCSDGPCNNNTSC.....CDITYCTGDSGCGPMLHK 55

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 3504750

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications_NA:
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	332	100.0	2268 9 US-09-809-790-1	Sequence 1, Appl1
3	332	100.0	2268 10 US-09-809-617-1	Sequence 1, Appl1
4	332	100.0	2268 10 US-10-260-506-1	Sequence 1, Appl1
5	332	100.0	2499 9 US-10-202-675-2	Sequence 2, Appl1
6	332	100.0	4043 4 US-09-824-129-2	Sequence 2, Appl1
7	332	100.0	4043 12 US-10-359-464-2	Sequence 2, Appl1
8	332	100.0	4720 12 US-10-260-506-9	Sequence 9, Appl1
9	325	97.9	494 11 US-09-918-995-22101	Sequence 22101, A
10	285	85.8	2088 9 US-09-809-790-3	Sequence 3, Appl1
11	285	85.8	2088 10 US-09-809-617-3	Sequence 3, Appl1
12	285	85.8	2088 12 US-10-260-506-3	Sequence 3, Appl1
13	285	85.8	2127 12 US-10-260-506-11	Sequence 11, Appl1
14	213	64.2	494 9 US-09-918-995-2610	Sequence 2610, Ap
15	185	55.7	1674 9 US-09-792-200B-15	Sequence 15, Appl1
16	185	55.7	2604 9 US-10-202-675-5	Sequence 1, Appl1
17	168.5	50.8	1638 9 US-09-792-200B-7	Sequence 7, Appl1
18	168.5	50.8	2720 12 US-10-101-510-230	Sequence 230, App
19	168.5	50.8	2740 10 US-09-880-107-3359	Sequence 3359, Ap
20	168.5	50.8	2740 12 US-10-101-510-418	Sequence 418, App
21	168.5	50.8	2968 13 US-10-014-501-1	Sequence 1, Appl1
22	167	50.3	2373 12 US-10-156-028-1	Sequence 1, Appl1
23	167	50.3	2695 12 US-10-137-870-203	Sequence 203, App
24	167	50.3	2695 12 US-10-140-018-203	Sequence 203, App
25	167	50.3	2695 12 US-10-140-021-203	Sequence 203, App
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27	167	50.3	2695 12 US-10-140-071-203	Sequence 203, App
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37	167	50.3	2695 12 US-10-142-767-203	Sequence 203, App
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45	167	50.3	2695 12 US-10-145-823-203	Sequence 203, App

ALIGNMENTS

RESULT 1
US-09-792-200B-17
Sequence 17, Application US/09792200B
Patent No. US20020042368A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Fanslow, William C.
APPLICANT: Poindexter, Kurt
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: INTEGRIN ANTAGONISTS
FILE REFERENCE: 2958-A
CURRENT APPLICATION NUMBER: US/09/792, 200B
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/184, 865
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent version 3.1
SEQ ID NO 17
LENGTH: 1668
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion Construct
NAME/KEY: CDS

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/ LOCATION: (25)..(1647)
/ OTHER INFORMATION:
US-09-792-200B-17

Alignment Scores:
Pred. No.: 1,22e-36 Length: 1668
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-792-200B-17 (1-1668)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrsCys 20
DB 172 TGTTCCTCTCCACAGGGGCTCCTGACGACGAGGGCCCTGCTGTAACATATCTCATGT 231
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
DB 232 CTTTTCAGCCACGAGGGATGAAATGCCGGATGCTGTGAACGAGTGTGATTAATCTGAA 291
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
DB 292 TATTGTACTGGAGACTCTGTGTCAGTCCACCAAAATCTTCATTAAG 336

RESULT 2
US-09-809-790-1
/ Sequence 1, Application US/09809790
/ Patent No. US20020072102A1
/ GENERAL INFORMATION:
/ APPLICANT: Shepard, Paul O.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Deisher, Theresa A.
/ APPLICANT: Bishop, Paul D.
/ TITLE OF INVENTION: DISINTEGRIN HOMOLOG
/ FILE REFERENCE: 98-29
/ CURRENT APPLICATION NUMBER: US/09/809,790
/ CURRENT FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 09/351,414
/ PRIOR FILING DATE: 1999-07-09
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 2268
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)...(2090)
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(2268)
/ OTHER INFORMATION: n = A,T,C or G
US-09-809-790-1

Alignment Scores:
Pred. No.: 1,79e-36 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-809-790-1 (1-2268)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrsCys 20
DB 1227 TGTTCCTCTCCACAGGGGCTCCTGACGACGAGGGCCCTGCTGTAACATATCTCATGT 1286
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
DB 1287 CTTTTCAGCCACGAGGGATGAAATGCCGGATGCTGTGAACGAGTGTGATTAATCTGAA 1346
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
DB 1347 TATTGTACTGGAGACTCTGTGTCAGTCCACCAAAATCTTCATTAAG 1391
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QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
DB 1347 TATTGTACTGGAGACTCTGTGTCAGTCCACCAAAATCTTCATTAAG 1391

RESULT 3
US-09-809-617-1
/ Sequence 1, Application US/09809617
/ Patent No. US20020137178A1
/ GENERAL INFORMATION:
/ APPLICANT: Shepard, Paul O.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Deisher, Theresa A.
/ APPLICANT: Bishop, Paul D.
/ TITLE OF INVENTION: DISINTEGRIN HOMOLOG
/ FILE REFERENCE: 98-29
/ CURRENT APPLICATION NUMBER: US/09/809,617
/ CURRENT FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: US/09/351,414
/ PRIOR FILING DATE: 1999-07-09
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 2268
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)...(2090)
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(2268)
/ OTHER INFORMATION: n = A,T,C or G
US-09-809-617-1

Alignment Scores:
Pred. No.: 1,79e-36 Length: 2268
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-809-617-1 (1-2268)

QY 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrsCys 20
DB 1227 TGTTCCTCTCCACAGGGGCTCCTGACGACGAGGGCCCTGCTGTAACATATCTCATGT 1286
QY 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
DB 1287 CTTTTCAGCCACGAGGGATGAAATGCCGGATGCTGTGAACGAGTGTGATTAATCTGAA 1346
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
DB 1347 TATTGTACTGGAGACTCTGTGTCAGTCCACCAAAATCTTCATTAAG 1391

RESULT 4
US-10-260-506-1
/ Sequence 1, Application US/10260506
/ Publication No. US20030153064A1
/ GENERAL INFORMATION:
/ APPLICANT: Shepard, Paul O.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Deisher, Theresa A.
/ APPLICANT: Bishop, Paul D.
/ APPLICANT: Taft, David W.
/ TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
/ FILE REFERENCE: 98-29C1
/ CURRENT APPLICATION NUMBER: US/10/260,506
/ CURRENT FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: 60/092,371
/ PRIOR FILING DATE: 1998-07-10
/ PRIOR APPLICATION NUMBER: 60/147,410
/ PRIOR FILING DATE: 1999-08-05
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PRIOR APPLICATION NUMBER: 09/351,414
 PRIOR FILING DATE: 1999-07-09
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 2268
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (3)...(2090)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(2268)
 OTHER INFORMATION: n = A,T,C or G
 US-10-260-506-1

Alignment Scores:
 Pred. No.: 1.79e-36 Length: 2268
 Score: 332.00 Matches: 55
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-10-260-506-1 (1-2268)

Qy 1 CysSerLeuSerArgGlyAlaHisCysSerAspGlyProCysGlyAsnAsnThrSerCys 20

Db 1227 TGTTCCTCTCCACGGGGCTCACTGCAGCGGGCCCTGCTGTAAACAATACCTCATGT 1286

Qy 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

Db 1287 CTTTTCAGCCACGAGGATGATGATGCGGGATCTGTGAACGATGATATTACTGAA 1346

Qy 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55

Db 1347 TATTGTACTGAGACTCTGTGCTAGTCCACCAATCTTCAATAG 1391

RESULT 5

US-10-202-675-2
 Sequence 2, Application US/10202675
 Publication No. US20030100091A1
 GENERAL INFORMATION:
 APPLICANT: Cerretti, Douglas P.
 TITLE OF INVENTION: SVPH3-13 DNA AND POLYPEPTIDES
 FILE REFERENCE: 03260, 0051-00304
 CURRENT APPLICATION NUMBER: US/10/202,675
 PRIOR FILING DATE: 2002-07-23
 PRIOR APPLICATION NUMBER: US/09/634,252
 PRIOR FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: 60/074,310
 PRIOR FILING DATE: 1998-02-11
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 2499
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-202-675-2

Alignment Scores:
 Pred. No.: 2.03e-36 Length: 2499
 Score: 332.00 Matches: 55
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-10-202-675-2 (1-2499)

Qy 1 CysSerLeuSerArgGlyAlaHisCysSerAspGlyProCysGlyAsnAsnThrSerCys 20

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 Qy 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40
 Db 1654 CTTTTCAGCCACGAGGATGATGATGCGGGATGCTGTGAACGATGATATTACTGAA 1713
 Qy 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55
 Db 1714 TATTGTACTGAGACTCTGTGCTAGTCCACCAATCTTCAATAG 1758

RESULT 6

US-09-824-129-2
 Sequence 2, Application US/09824129
 Patent No. US2002001840A1
 GENERAL INFORMATION:
 APPLICANT: Lopez-Otin, Carlos
 APPLICANT: Miguel, Santiago Cal
 APPLICANT: Freije, Jose Maria Perez
 APPLICANT: Garcia, Jose Manuel Lopez
 APPLICANT: Bianchi, Albert Bernard
 APPLICANT: Trail, Pamela
 TITLE OF INVENTION: Methods and Compositions for Modulating
 TITLE OF INVENTION: Integrin-mediated Cell-Cell Interactions
 FILE REFERENCE: D0015-NP
 CURRENT APPLICATION NUMBER: US/09/824,129
 PRIOR FILING DATE: 2001-04-02
 PRIOR APPLICATION NUMBER: 60/194,164
 PRIOR FILING DATE: 2000-04-03
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 4043
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-824-129-2

Alignment Scores:
 Pred. No.: 3.72e-36 Length: 4043
 Score: 332.00 Matches: 55
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-824-129-2 (1-4043)

Qy 1 CysSerLeuSerArgGlyAlaHisCysSerAspGlyProCysGlyAsnAsnThrSerCys 20

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Qy 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

Db 2670 CTTTTCAGCCACGAGGATGATGATGCGGGATGCTGTGAACGATGATATTACTGAA 2729

Qy 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIlys 55

Db 2730 TATTGTACTGAGACTCTGTGCTAGTCCACCAATCTTCAATAG 2774

RESULT 7

US-10-359-464-2
 Sequence 2, Application US/10359464
 Publication No. US20030143692A1
 GENERAL INFORMATION:
 APPLICANT: Lopez-Otin, Carlos
 APPLICANT: Miguel, Santiago Cal
 APPLICANT: Freije, Jose Maria Perez
 APPLICANT: Garcia, Jose Manuel Lopez
 APPLICANT: Bianchi, Albert Bernard
 APPLICANT: Trail, Pamela
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING INTEGRIN-MEDIATED
 TITLE OF INVENTION: CELL-CELL INTERACTIONS
 FILE REFERENCE: D0015 DIV
 CURRENT APPLICATION NUMBER: US/10/359,464

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; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 09/824,129
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/194,164
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.2
; SEQ ID NO 2
; LENGTH: 4043
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-359-464-2

Alignment Scores:
Pred. No.: 3,72e-36 Length: 4043
Score: 332.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-10-359-464-2 (1-4043)

QY 1 CysSerLeuSerAenGlyAlaHisCySerAaspGlyProCyCyAsnAsnThSerCys 20
Db 2610 TGTTCCTCTCCAAACGGGGCTCACTGCAGCGACGCGGCGCTGTAAACAATACCTCATGT 2669

QY 21 LeuPheGlnProAArgGlyTYrGluCyArgAspAlaValaAenGluCyAspIleThGlu 40
Db 2670 CTTTTCAGCCACGAGGGATGAATGCGGGATGCTGTGAAGAGATGTGATATTACTAA 2729

QY 41 TYrCyThrGlyAaspSerGlyGlnCySppProAsnLeuHisLys 55
Db 2730 TATTACTGGAGACTGTGTGAGTGCACCAATCTTCAATAG 2774

RESULT 8
US-10-260-506-9
; Sequence 9, Application US/10260506
; Publication No. US20030153064A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Desher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/10/260,506
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 4720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2129)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4720)
; OTHER INFORMATION: n = A,T,C or G
US-10-260-506-9

Alignment Scores:
Pred. No.: 4,53e-36 Length: 4720
Score: 332.00 Matches: 55
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-10-260-506-9 (1-4720)

QY 1 CysSerLeuSerAenGlyAlaHisCySerAaspGlyProCyCyAsnAsnThSerCys 20
Db 1227 TGTTCCTCTCCAAACGGGGCTCACTGCAGCGACGCGGCGCTGTAAACAATACCTCATGT 1286

QY 21 LeuPheGlnProAArgGlyTYrGluCyArgAspAlaValaAenGluCyAspIleThGlu 40
Db 1287 CTTTTCAGCCACGAGGGATGAATGCGGGATGCTGTGAAGAGATGTGATATTACTGAA 1346

QY 41 TYrCyThrGlyAaspSerGlyGlnCySppProAsnLeuHisLys 55
Db 1347 TATTACTGGAGACTGTGTGAGTGCACCAATCTTCAATAG 1391

RESULT 9
US-09-918-995-22101
; Sequence 22101, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22101
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22101

Alignment Scores:
Pred. No.: 2,49e-36 Length: 494
Score: 325.00 Matches: 54
Percent Similarity: 98.18% Conservative: 0
Best Local Similarity: 98.18% Mismatches: 1
Query Match: 97.89% Indels: 0
DB: 11 Gaps: 0

US-09-634-252a-4_COPY_532_586 (1-55) x US-09-918-995-22101 (1-494)

QY 1 CysSerLeuSerAenGlyAlaHisCySerAaspGlyProCyCyAsnAsnThSerCys 20
Db 234 TGTTCCTCTCCAAACGGGGCTCACTGCAGCGACGCGGCGCTGTAAACAATACCTCATGT 293

QY 21 LeuPheGlnProAArgGlyTYrGluCyArgAspAlaValaAenGluCyAspIleThGlu 40
Db 294 CTTTTCAGCCACGAGGGATGAATGCGGGATGCTGTGAAGAGATGTGATATTACTGAA 353

QY 41 TYrCyThrGlyAaspSerGlyGlnCySppProAsnLeuHisLys 55
Db 354 TATTACTGGAGACTGTGTGAGTGCACCAATCTTCAATAG 398

RESULT 10
US-09-809-790-3
; Sequence 3, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Baindur, Nand
```

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1  APPLICANT:  Delsner, Theresa A.
2  APPLICANT:  Bishop, Paul D.
3  TITLE OF INVENTION:  DISINTEGRIN HOMOLOG
4  FILE REFERENCE:  98-29
5  CURRENT APPLICATION NUMBER:  US/09/809,790
6  CURRENT FILING DATE:  2001-03-16
7  PRIOR APPLICATION NUMBER:  09/351,414
8  PRIOR FILING DATE:  1999-07-09
9  NUMBER OF SEQ ID NOS:  13
10 SOFTWARE:  FASTSEQ for Windows Version 3.0
11 SEQ ID NO 3
12 LENGTH:  2088
13 TYPE:  DNA
14 ORGANISM:  Artificial Sequence
15 FEATURE:
16 NAME INFORMATION:  zdn1c1 amino acid degenerate sequence
17 NAME/KEY:  variation
18 LOCATION:  (1)...(2088)
19 OTHER INFORMATION:  n is any nucleotide
20 NAME/KEY:  misc feature
21 LOCATION:  (1)...(2088)
22 OTHER INFORMATION:  n = A,T,C or G
23 US-09-809-790-3

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Alignment Scores:

Pred. No.:	6,19e-30	length:	2068
Score:	285.00	Matches:	45
Percent Similarity:	81.82%	Conservative:	0
Best Local Similarity:	81.82%	Mismatches:	10
Query Match:	85.84%	Indels:	0
DB:	9	Gaps:	0

US-09-634-252A-4_COPY_532_586 (1-55) X US-09-809-790-3 (1-2,088)

Qy 1 CysSerLeuSerArgGlyAlaAlaHisGlySerSerArgGlyProCysCysAsnAsnThrSerGly 20
 Db 1225 TGYSSNYNTWNSNAALGAGGNCACAYGYMSNGAYGGNCCTGTGTAAAYAAACNWSNTGY 1284
 Qy 21 LeuPheGlnProCArgGlyTyrGluCysArgAspAlaValaLaangluCysAspGluethGlu 40
 Db 1285 YTNNTTTCARCCMGNGGNTAAGARGYMGNGAYGGNGTNAALVGAATGYGAAYATHACNGAR 1344
 Qy 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisIleGly 55
 Db 1345 TATGTACGAGGNGAYMSNGNCARTGTGCNCCTCAAYATYNNCAVAA. 1389

Search completed: October 21, 2003, 14:49:55
Job time : 145.094 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2003, 10:10:45 ; Search time 110.692 Seconds
(without alignments)
83.207 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586

Perfect score: 332
Sequence: 1 CSLSNGAHCSDBGCCNNTSC.....CDITEYCTGDSGCCPPNLHK 55

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubppaa/PCRT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppaa/US10C_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	100.0	540	9	US-09-792-200B-18
2	332	100.0	696	9	US-09-809-790-2
3	332	100.0	696	10	US-09-809-617-2
4	332	100.0	696	12	US-10-260-506-2
5	332	100.0	709	12	US-10-260-506-10
6	332	100.0	832	9	US-09-824-129-3
7	332	100.0	832	12	US-10-359-464-3
8	332	100.0	832	15	US-10-202-675-4
9	185	55.7	542	9	US-09-792-200B-16
10	185	55.7	867	15	US-10-202-675-6
11	172	51.8	76	11	US-09-877-843-88
12	168.5	50.8	522	9	US-09-792-200B-8
13	168.5	50.8	814	14	US-10-014-501-4
14	168.5	50.8	855	14	US-10-014-501-2
15	167	50.3	790	12	US-10-137-870-204

16	167	50.3	790	12	US-10-140-018-204	Sequence 204, App
17	167	50.3	790	12	US-10-140-021-204	Sequence 204, App
18	167	50.3	790	12	US-10-140-024-204	Sequence 204, App
19	167	50.3	790	12	US-10-140-471-204	Sequence 204, App
20	167	50.3	790	12	US-10-140-807-204	Sequence 204, App
21	167	50.3	790	12	US-10-140-922-204	Sequence 204, App
22	167	50.3	790	12	US-10-140-924-204	Sequence 204, App
23	167	50.3	790	12	US-10-140-926-204	Sequence 204, App
24	167	50.3	790	12	US-10-141-698-204	Sequence 204, App
25	167	50.3	790	12	US-10-141-702-204	Sequence 204, App
26	167	50.3	790	12	US-10-141-704-204	Sequence 204, App
27	167	50.3	790	12	US-10-142-421-204	Sequence 204, App
28	167	50.3	790	12	US-10-142-432-204	Sequence 204, App
29	167	50.3	790	12	US-10-142-767-204	Sequence 204, App
30	167	50.3	790	12	US-10-143-033-204	Sequence 204, App
31	167	50.3	790	12	US-10-144-994-204	Sequence 204, App
32	167	50.3	790	12	US-10-145-628-204	Sequence 204, App
33	167	50.3	790	12	US-10-145-631-204	Sequence 204, App
34	167	50.3	790	12	US-10-145-633-204	Sequence 204, App
35	167	50.3	790	12	US-10-145-746-204	Sequence 204, App
36	167	50.3	790	12	US-10-145-748-204	Sequence 204, App
37	167	50.3	790	12	US-10-145-823-204	Sequence 204, App
38	167	50.3	790	12	US-10-145-826-204	Sequence 204, App
39	167	50.3	790	12	US-10-145-870-204	Sequence 204, App
40	167	50.3	790	12	US-10-145-876-204	Sequence 204, App
41	167	50.3	790	12	US-10-145-959-204	Sequence 204, App
42	167	50.3	790	12	US-10-146-724-204	Sequence 204, App
43	167	50.3	790	12	US-10-146-725-204	Sequence 204, App
44	167	50.3	790	12	US-10-146-795-204	Sequence 204, App
45	167	50.3	790	12	US-10-147-495-204	Sequence 204, App

ALIGNMENTS

RESULT 1
US-09-792-200B-18 Application US/09792200B
Sequence 18, Application US/09792200B
Patent No. US20020042368A1

GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Fanslow, William C.
APPLICANT: Poindexter, Kurt
APPLICANT: Cerretti, Douglas P.
APPLICANT: Black, Roy A.
TITLE OF INVENTION: INTEGRIN ANTAGONISTS
FILE REFERENCE: 2958-A
CURRENT APPLICATION NUMBER: US/09/792.200B
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 66/164,865
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 540
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion Construct

US-09-792-200B-18

Query Match 100.0%; Score 332; DB 9; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNGAHCSDBGCCNNTSCIFQPGYECRDVAVECDITEYCTGDSGCCPPNLHK 55
DB 50 CSLSNGAHCSDBGCCNNTSCIFQPGYECRDVAVECDITEYCTGDSGCCPPNLHK 104

RESULT 2
US-09-809-790-2
Sequence 2, Application US/09809790

Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-790-2

Query Match 100.0%; Score 332; DB 9; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.9e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 409 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 463

RESULT 3
US-09-809-617-2
; Sequence 2, Application US/09809617
; Patent No. US20020317178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-617-2

Query Match 100.0%; Score 332; DB 10; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.9e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 409 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 463

RESULT 4
US-10-260-506-2
; Sequence 2, Application US/10260506
; Publication No. US20030153064A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29CI

; CURRENT APPLICATION NUMBER: US/10/260,506
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-506-2

Query Match 100.0%; Score 332; DB 12; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.9e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 409 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 463

RESULT 5
US-10-260-506-10
; Sequence 10, Application US/10260506
; Publication No. US20030153064A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29CI
; CURRENT APPLICATION NUMBER: US/10/260,506
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-506-10

Query Match 100.0%; Score 332; DB 12; Length 709;
Best Local Similarity 100.0%; Pred. No. 1.9e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
DB 409 CSLSNAGHCSGDPCCNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 463

RESULT 6
US-09-824-129-3
; Sequence 3, Application US/09824129
; Patent No. US2002001840A1
; GENERAL INFORMATION:
; APPLICANT: Lopez-Otin, Carlos
; APPLICANT: Miguel, Santiago Cal
; APPLICANT: Freije, Jose Maria Perez
; APPLICANT: Garcia, Jose Manuel Lopez
; APPLICANT: Bianchi, Albert Bernard
; APPLICANT: Trall, Pamela

```
;; TITLE OF INVENTION: Methods and Compositions for Modulating
;; FILE REFERENCE: D0015-NP
;; CURRENT APPLICATION NUMBER: US/09/824,129
;; CURRENT FILING DATE: 2001-04-02
;; PRIOR APPLICATION NUMBER: 60/194,164
;; PRIOR FILING DATE: 2000-04-03
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 832
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-824-129-3

Query Match      100.0%; Score 332; DB 9; Length 832;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITEYCTGDSGCCPPNHLK 55
Db      532 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITEYCTGDSGCCPPNHLK 586
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RESULT 7
US-10-359-464-3
; Sequence 3, Application US/10359464
; Publication No. US20030143692A1
; GENERAL INFORMATION:
; APPLICANT: Lopez-Otin, Carlos
; APPLICANT: Migue, Santiago Cal
; APPLICANT: Freije, Jose Maria Perez
; APPLICANT: Garcia, Jose Manuel Lopez
; APPLICANT: Bianchi, Albert Bernard
; APPLICANT: Trail, Pamela
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING INTEGRIN-MEDIATED
; FILE REFERENCE: D0015 DIV
; CURRENT APPLICATION NUMBER: US/10/359,464
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 09/824,129
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/194,164
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-359-464-3

Query Match      100.0%; Score 332; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITEYCTGDSGCCPPNHLK 55
Db      532 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITEYCTGDSGCCPPNHLK 586
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RESULT 8
US-10-202-675-4
; Sequence 4, Application US/10202675
; Publication No. US20030100091A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES
; FILE REFERENCE: 03260.0051-00304
; CURRENT APPLICATION NUMBER: US/10/202,675
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/09/634,252
; PRIOR FILING DATE: 2000-08-07
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;; PRIOR APPLICATION NUMBER: 60/074,310
;; PRIOR FILING DATE: 1998-02-11
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 832
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-202-675-4
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Query Match      100.0%; Score 332; DB 15; Length 832;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITEYCTGDSGCCPPNHLK 55
Db      532 CSLSNGAHCSGDPCCNNTSCLFOPRGYECRDVAVECDITEYCTGDSGCCPPNHLK 586
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RESULT 9
US-09-792-200B-16
; Sequence 16, Application US/09792200B
; Patent No. US20020042368A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Fanslow, William C.
; APPLICANT: Poindexter, Kurt
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: INTEGRIN ANTAGONISTS
; FILE REFERENCE: 2958-A
; CURRENT APPLICATION NUMBER: US/09/792,200B
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/184,865
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-792-200B-16
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; Sequence 6, Application US/10202675
; Publication No. US20030100091A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES
; FILE REFERENCE: 03260.0051-00304
; CURRENT APPLICATION NUMBER: US/10/202,675
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/09/634,252
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/074,310
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 867
; TYPE: PRT
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: October 21, 2003, 10:10:45 ; Search time 209.308 Seconds
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83.207 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	630	100.0	696	10	US-09-809-617-2 Sequence 2, Appli
3	630	100.0	696	12	US-10-260-506-2 Sequence 2, Appli
4	630	100.0	709	12	US-10-260-506-10 Sequence 10, Appli
5	630	100.0	832	9	US-09-824-129-3 Sequence 3, Appli
6	630	100.0	832	12	US-10-359-464-3 Sequence 3, Appli
7	630	100.0	832	15	US-10-202-675-4 Sequence 4, Appli
8	586	93.0	540	9	US-09-792-200B-18 Sequence 18, Appli
9	363.5	57.7	867	15	US-10-202-675-6 Sequence 6, Appli
10	338.5	53.7	542	9	US-09-792-200B-16 Sequence 16, Appli
11	292	46.3	802	12	US-10-177-308-2 Sequence 2, Appli
12	292	46.3	812	12	US-09-834-597-363 Sequence 363, App
13	292	46.3	812	12	US-10-177-308-4 Sequence 4, App
14	292	46.3	813	12	US-10-199-672-466 Sequence 466, App
15	292	46.3	813	12	US-10-187-749-466 Sequence 466, App

16	292	46.3	813	12	US-10-194-457-466	Sequence 466, App
17	292	46.3	813	12	US-10-184-642-466	Sequence 466, App
18	292	46.3	813	12	US-10-196-747-466	Sequence 466, App
19	292	46.3	813	12	US-10-173-689-466	Sequence 466, App
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26	292	46.3	813	12	US-10-173-707-466	Sequence 466, App
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35	292	46.3	813	12	US-10-175-745-466	Sequence 466, App
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37	292	46.3	813	12	US-10-175-751-466	Sequence 466, App
38	292	46.3	813	12	US-10-175-754-466	Sequence 466, App
39	292	46.3	813	12	US-10-176-480-466	Sequence 466, App
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41	292	46.3	813	12	US-10-176-754-466	Sequence 466, App
42	292	46.3	813	12	US-10-176-755-466	Sequence 466, App
43	292	46.3	813	12	US-10-176-759-466	Sequence 466, App
44	292	46.3	813	12	US-10-176-920-466	Sequence 466, App
45	292	46.3	813	12	US-10-176-922-466	Sequence 466, App

ALIGNMENTS

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US-09-809-790-2
; Sequence 2, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Desher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-790-2

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Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 373 PTKLFEPTGCGNGYVAGEEBCDGFHVECYGLCKKCSLSNGAHCSDGPCNNNTSCLP 432
QY 61 RGYECRDVAVNECDITTEYCTGDSGOCPPNLHKQDYACNONGRC 104
DB 433 RGYECRDVAVNECDITTEYCTGDSGOCPPNLHKQDYACNONGRC 476
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US-09-809-617-2

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; Sequence 2, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baird, Nand O.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-617-2
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; Sequence 2, Application US/10260506
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baird, Nand O.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/10/260,506
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
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; Sequence 10, Application US/10260506
; Patent No. US20030153064A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baird, Nand O.
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOGUE, MAHBP
; FILE REFERENCE: 98-29C1
; CURRENT APPLICATION NUMBER: US/10/260,506
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/092,371
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/147, 410
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-506-10
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RESULT 5
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; Sequence 3, Application US/09824129
; Patent No. US20020001840A1
; GENERAL INFORMATION:
; APPLICANT: Lopez-Otin, Carlos
; APPLICANT: Miguel, Santiago Cal
; APPLICANT: Freije, Jose Maria Perez
; APPLICANT: Garcia, Jose Manuel Lopez
; APPLICANT: Bianchi, Albert Bernard
; APPLICANT: Trall, Pamela
; TITLE OF INVENTION: Methods and Compositions for Modulating
; TITLE OF INVENTION: Integrin-mediated Cell-Cell Interactions
; FILE REFERENCE: D0015-NP
; CURRENT APPLICATION NUMBER: US/09/824,129
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/194,164
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Homo sapiens
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RESULT 10
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 ; Sequence 16, Application US/09792200B
 ; Patent No. US20020042368A1

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Farnsworth, William C.

APPLICANT: Poindexter, Kurt

APPLICANT: Cerretti, Douglas P.

APPLICANT: Black, Roy A.

TITLE OF INVENTION: INTEGRIN ANTAGONISTS

FILE REFERENCE: 2958-A

CURRENT APPLICATION NUMBER: US/09/792,200B

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: US 60/184,865

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 16

LENGTH: 542

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion Construct

US-09-792-200B-16

Query Match 53.7%; Score 338.5; DB 9; Length 542;

Best Local Similarity 57.0%; Pred. No. 1.5e-22;

Matches 57; Conservative 12; Mismatches 26; Indels 5; Gaps 2;

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QY 65 CRDANECDITEYCTGDSGQCPNHLKODGYACNONOGRG 104
 DB 79 CREAVNDCDIRETCGNSQCAPNHLKMDGYS CDVGQIG 118

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	213	64.2	1464	1	US-08-484-355-5
6	213	64.2	2913	1	US-08-243-542-7
7	213	64.2	2913	1	US-08-477-407-7
8	213	64.2	2913	1	US-08-484-355-7
9	213	64.2	2923	1	US-08-243-542-6
10	213	64.2	2923	1	US-08-477-407-6
11	213	64.2	2923	1	US-08-484-355-6
12	213	64.2	3183	1	US-08-243-542-8

13	213	64.2	3183	1	US-08-477-407-8	Sequence 8, Appl1
14	213	64.2	3183	1	US-08-484-355-8	Sequence 8, Appl1
15	168.5	50.8	2968	3	US-09-813-819-1	Sequence 1, Appl1
16	168.5	50.8	2968	4	US-09-920-048-1	Sequence 1, Appl1
17	160	48.2	1507	4	US-09-280-116-122	Sequence 122, App
18	160	48.2	3431	4	US-09-632-098-1	Sequence 1, Appl1
19	160	48.2	3468	4	US-09-632-098-3	Sequence 3, Appl1
20	153	46.1	1463	5	PCT-US93-05640-10	Sequence 10, Appl1
21	152	45.8	2373	1	US-08-264-101-1	Sequence 1, Appl1
22	152	45.8	2373	2	US-08-765-243-1	Sequence 1, Appl1
23	152	45.8	2373	5	PCT-US95-07295-1	Sequence 1, Appl1
24	152	45.8	2573	5	US-08-765-243-7	Sequence 7, Appl1
25	152	45.8	2650	5	PCT-US95-07295-7	Sequence 7, Appl1
26	149	44.9	485	4	US-09-280-116-39	Sequence 39, Appl1
27	147	44.3	1851	4	US-09-608-790-2	Sequence 2, Appl1
28	145	43.7	2169	4	US-09-617-145-1	Sequence 1, Appl1
29	144.5	43.5	3994	4	US-09-738-946-7	Sequence 7, Appl1
30	144	43.4	1768	1	US-08-264-101-3	Sequence 3, Appl1
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baird, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ. ID NOS.: 13
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(2090)
; NAME/KEY: misc_feature
; LOCATION: (1)..(2268)
; OTHER INFORMATION: n = A,T,C or G
US-09-351-414-1
Alignment Scores:
Pred. No.: 2.3e-33
Score: 332.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 2268
Matches: 55
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) X US-09-351-414-1 (1-2268)

Qy 1 CysSerLeuSerAsgGlyAlaHisCysSerAsgGlyProCysCysAsnAsnThSerCys 20
Db 1227 TGTTCCTCTCCACAGCGGGCTGCTGACGCGCGCCCTGCTGTAACATACCTCATGT 1286
Qy 21 LeuPheGlnProAArgGlyTyrGluCysArgAspAlaValaGluCysAsp11eThrGlu 40
Db 1287 CTTTTCGCGCAGCGGGGTATGAAAGCCGGAGTGTGAAAGAGTGTGATATTACTGAA 1346
Qy 41 TyrCysThrGlyAaspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1347 TATGTACTGAGACTCTGCTGACGTCGCCCAATCTTCATTAAG 1391
RESULT 2
US-09-351-414-3
Sequence 3, Application US/09351414
Patent No. 6265199
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baidur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2088
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zdn1 amino acid degenerate sequence
FEATURE:
NAME/KEY: variation
LOCATION: (1)...(2088)
OTHER INFORMATION: n is any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(2088)
OTHER INFORMATION: n = A,T,C or G
US-09-351-414-3
Alignment Scores:
Pred. No.: 2,31e-27 Length: 2088
Score: 285.00 Matches: 45
Percent Similarity: 81.82% Conservative: 0
Best Local Similarity: 81.82% Mismatches: 10
Query Match: 85.84% Indels: 0
DB: 3 Gaps: 0
US-09-634-252a-4_COPY_532_586 (1-55) x US-09-351-414-3 (1-2088)
Qy 1 CysSerLeuSerAsgGlyAlaHisCysSerAsgGlyProCysCysAsnAsnThSerCys 20
Db 1225 TGYMSNTYTMGNAAYAGGNCACATGYGWSNGAYGAGNCNTGTGTAAYAAACNMSNTGY 1284
Qy 21 LeuPheGlnProAArgGlyTyrGluCysArgAspAlaValaGluCysAsp11eThrGlu 40
Db 1285 YTNNTTCARCCNMGNGNTATGARTGNGNGAYGAGNTAAAGARTGGAAYATTAACNGAR 1344
Qy 41 TyrCysThrGlyAaspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1345 TATGTACNGGNGAYWSNGNCARTGTCCNCCNAAYTNCAIYAR 1389
RESULT 3
US-08-243-542-5
Sequence 5, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU

TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1464
US-08-243-542-5
Alignment Scores:
Pred. No.: 2.83e-18 Length: 1464
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 1 Gaps: 1
US-09-634-252a-4_COPY_532_586 (1-55) x US-08-243-542-5 (1-1464)
Qy 1 CysSerLeuSerAsgGlyAlaHisCysSerAsgGlyProCysCysAsnAsnThSerCys 20
Db 1111 TGCACCTGACTCAGCAGCCCATGTGACGACGCGCTGCTGCGCCC-----TGC 1164
Qy 21 LeuPheGlnProAArgGlyTyrGluCysArgAspAlaValaGluCysAsp11eThrGlu 40
Db 1165 AAGTACGACACCGGGGTGTCTCTGCGAGAGCCCTGAACAGTGCACATGCGCGAG 1224
Qy 41 TyrCysThrGlyAaspSerGlyGlnCysProProAsnLeuHisLys 55

Db 1225 ACTGCACCGGGACTAGCCAGTCCCGCCTAAGCTGACAA3 1269

RESULT 4

US-08-477-407-5

Sequence 5, Application US/08477407
Patent No. 5631351

GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994

ATTORNEY/AGENT INFORMATION:

NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 1464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1464

US-08-477-407-5

Alignment Scores:

Pred. No.: 2,83e-18 Length: 1464
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 1 Gaps: 1

US-09-634-252a-4_copy_532_586 (1-55) x US-08-477-407-5 (1-1464)

Qy 1 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20

Db 1111 TGCACCTGACTCAGCAGCGCATGTGTCAGCGAGCGGTCTGCTGTCCGCC-----TGC 1164

Qy 21 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 40

Db 1165 AAGTACGAAACACGAGCGGTGTCTCCGCCGAGAGCGCTGAACGAGTCGACATCGCGAG 1224

Qy 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55

Db 1225 ACTGCACCGGGACTAGCCAGTCCCGCCTAAGCTGACAA3 1269

RESULT 5

US-08-484-355-5

Sequence 5, Application US/08484355
Patent No. 5705341

GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994

ATTORNEY/AGENT INFORMATION:

NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 1464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1464

US-09-634-252a-4_copy_532_586 (1-55) x US-08-477-407-5 (1-1464)

RESULT 9
US-08-243-542-6
Sequence 6, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
NUMBER OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..27
NAME/KEY: 3' UTR
LOCATION: 1600..2923
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1599
US-08-243-542-6
Alignment Scores:
Pred. No.: 6, 9e-18 Length: 2923
Score: 213.00 Matches: 36
Percent Similarity: 76.36% Conservative: 6
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 64.16% Indels: 2
DB: 1 Gaps: 1

US-09-634-252A-4_COPY_532_586 (1-55) x US-08-243-542-6 (1-2923)
QY 1 CysSerLeuSerArgAnglyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 20
Db 1159 TGCACCTGACTACGACGCGCATGTGCACGCGGCTGTCTGTCCGCCG-----TGC 1212
QY 21 LeuPheGlnProAArgGlyTyrGluCysArgAspAlaValaAngluCysAspIleThrGlu 40
Db 1213 AAGTACGACCAACGCGGGGTGTCTCTGCGCGAGAGGCCCGTGAACGAGTGGCATCGCGGAG 1272
QY 41 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLys 55
Db 1273 ACCTGACCGGGGACTGACGCGAGTGCCTAAGCTGACCAAG 1317
RESULT 10
US-08-477-407-6
Sequence 6, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
NUMBER OF INVENTION: ENCODING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:

NAME/KEY: 5' UTR
 LOCATION: 1..27
 FEATURE:
 NAME/KEY: 3' UTR
 LOCATION: 1600..2923
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 28..1599
 US-08-477-407-6

Alignment Scores:

Pred. No.:	6.9e-18	Length:	2923
Score:	213.00	Matches:	36
Percent Similarity:	76.36%	Conservative:	6
Best Local Similarity:	65.45%	Mismatches:	11
Query Match:	64.16%	Indels:	2
DB:	1	Gaps:	1

US-09-634-252a-4_COPY_532_586 (1-55) x US-08-477-407-6 (1-2923)

QY	1	CysSerLeuSerAenGlyAlaHisCysSerAenGlyProCysCyAanAanThrSerCys	20
DB	1159	TGCACCTGACTCAGACGCCATGTGACGACGCGGCTCTGTCGCGCCG-----TGC	1212
QY	21	LeuPheGlnProAArgGlyTyGluCysAArgAalaValAenGluCysAspIleThrGlu	40
DB	1213	AAGTACGAAACCGCGGCTGTCTCTGCGGAGAGCCCGTGAACGAGTGGACATCGCGGAG	1272
QY	41	TyrCysThrGlyAenPheSerGlyGlnCysProProAenLeuHisIle	55
DB	1273	ACCTGACCGGCGGACTCTAAGCCAGTGCCTAACCCTGACCAAG	1317

Search completed: October 21, 2003, 12:03:47
 Job time : 37.8616 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2003, 10:06:05 ; Search time 12.7987 Seconds
(without alignments)
181.822 Million cell updates/sec

Title: US-09-634-252a-4_COPY_532_586

Perfect score: 332

Sequence: 1 CSLSNGAHCSGDCPCNNNTSC.....CDITEYCTGDSGOCPPNLHK 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 323717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	213	64.2	488	1	US-08-243-542-1
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4	213	64.2	488	1	US-08-484-355-1
5	213	64.2	524	1	US-08-243-542-2
6	213	64.2	524	1	US-08-477-407-2
7	213	64.2	524	1	US-08-484-355-2
8	213	64.2	670	1	US-08-243-542-3
9	213	64.2	670	1	US-08-477-407-3
10	213	64.2	670	1	US-08-484-355-3
11	213	64.2	769	1	US-08-243-542-4
12	213	64.2	769	1	US-08-477-407-4
13	213	64.2	769	1	US-08-484-355-4
14	168.5	50.8	814	3	US-09-813-819-4
15	168.5	50.8	814	3	US-09-920-048-4
16	168.5	50.8	855	3	US-09-813-819-2
17	168.5	50.8	855	3	US-09-920-048-2
18	160	48.2	802	4	US-09-632-098-2
19	160	48.2	812	4	US-09-632-098-4
20	152	45.8	651	1	US-08-264-101-2
21	152	45.8	651	2	US-08-765-243-2
22	152	45.8	651	5	PCT-US95-07295-2
23	152	45.8	734	2	US-08-765-243-8
24	152	45.8	734	5	PCT-US95-07295-8
25	147	44.3	616	4	US-09-608-790-1
26	145	43.7	722	4	US-09-617-145-2
27	144.5	43.5	781	4	US-09-738-946-8

28	144	43.4	457	1	US-08-264-101-4	Sequence 4, Appli
29	144	43.4	457	2	US-08-765-243-4	Sequence 4, Appli
30	144	43.4	457	5	PCT-US95-07295-4	Sequence 4, Appli
31	144	43.4	735	2	US-08-765-243-6	Sequence 6, Appli
32	144	43.4	735	5	PCT-US95-07295-6	Sequence 6, Appli
33	141	42.5	50	5	PCT-US91-05640-16	Sequence 15, Appli
34	141	42.5	50	5	PCT-US91-05640-25	Sequence 15, Appli
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36	132.5	39.9	681	2	US-08-655-345-4	Sequence 4, Appli
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38	132.5	39.9	681	5	PCT-US96-08407-4	Sequence 4, Appli
39	132.5	39.9	698	4	US-09-727-169-4	Sequence 4, Appli
40	132.5	39.9	698	4	US-09-579-766A-4	Sequence 4, Appli
41	132.5	39.9	698	4	US-09-726-968-4	Sequence 4, Appli
42	132.5	39.9	807	2	US-08-655-345-2	Sequence 2, Appli
43	132.5	39.9	807	3	US-09-183-275-2	Sequence 2, Appli
44	132.5	39.9	807	5	PCT-US96-08407-2	Sequence 2, Appli
45	132.5	39.9	824	4	US-09-727-169-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-351-414-2
: Sequence 2, Application US/09351414
: Patent No. 6265199
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Balindur, Nand
: APPLICANT: Delisher, Theresa A.
: APPLICANT: Bishop, Paul D.
: TITLE OF INVENTION: DISINTEGRIN HOMOLOG
: FILE REFERENCE: 98-29
: CURRENT APPLICATION NUMBER: US/09/351,414
: CURRENT FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 696
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-351-414-2

Query Match      100.0%; Score 332; DB 3; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSLSNGAHCSGDCPCNNNTSCLPGRGYECRDVAVECDITEYCTGDSGOCPPNLHK 55
Db      409 CSLSNGAHCSGDCPCNNNTSCLPGRGYECRDVAVECDITEYCTGDSGOCPPNLHK 463

RESULT 2
US-08-243-542-1
: Sequence 1, Application US/08243542
: Patent No. 5552526
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: : EMI, MITSURU
: TITLE OF INVENTION: MDC PROTEINS AND DNAs
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THIEU, BOUTELL & TANIS P. C.
: STREET: 2026 Rambling Road
: CITY: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
```

OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain CDNA library
US-08-243-542-1

Query Match 64.2%; Score 213; DB 1; Length 488;
Best Local Similarity 65.5%; Pred. No. 6.6e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

OY 1 CSLSNGACSDGPPCCNNNTSCLFQPRGYECRDVNECDITTEYCTGSGCCPPLHK 55
Db 371 CTLTHDAMCSGDLCCRR--CKYEPBGVSCREAVNECDIAETCTGDSGCCPPLHK 423

RESULT 3
US-08-477-407-1
Sequence 1, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542

FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain CDNA library
US-08-477-407-1

Query Match 64.2%; Score 213; DB 1; Length 488;
Best Local Similarity 65.5%; Pred. No. 6.6e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

OY 1 CSLSNGACSDGPPCCNNNTSCLFQPRGYECRDVNECDITTEYCTGSGCCPPLHK 55
Db 371 CTLTHDAMCSGDLCCRR--CKYEPBGVSCREAVNECDIAETCTGDSGCCPPLHK 423

RESULT 4
US-08-484-355-1
Sequence 1, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904

FILED DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-484-355-1

Query Match 64.2%; Score 213; DB 1; Length 488;
Best Local Similarity 65.5%; Pred. No. 6,6e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

OY 1 CSLSNGHCSGDPCCNNTSCLPFGYECRDVAVNECDITETCTGSGCCPNNLHK 55
Db 371 CILTHDAMCSDGLCCRR--CKYEPBGVSCREAVNECDIAETCTGSSQCCPNNLHK 423

RESULT 5

US-08-243-542-2
Sequence 2, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549

REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-243-542-2

Query Match 64.2%; Score 213; DB 1; Length 524;
Best Local Similarity 65.5%; Pred. No. 7e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

OY 1 CSLSNGHCSGDPCCNNTSCLPFGYECRDVAVNECDITETCTGSDGSCPNNLHK 55
Db 378 CILTHDAMCSDGLCCRR--CKYEPBGVSCREAVNECDIAETCTGSSQCCPNNLHK 430

RESULT 6
US-08-477-407-2
Sequence 2, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain CDNA library
US-08-477-407-2

Query Match 64.2%; Score 213; DB 1; Length 524;
Best Local Similarity 65.5%; Pred. No. 7e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSLSNAGHSDGPCNNNTSCLEFOPRGYECRDVNECDITEYCTGDSGCCPPLHK 55
Db 378 CULTHDMCSDGLCCRR--CKIEPRGVSCREAVNECDIAETCTGDSGCCPPLHK 430

RESULT 7
US-08-484-355-2
Sequence 2, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
LIBRARY: human fetal brain CDNA library
US-08-484-355-2

Query Match 64.2%; Score 213; DB 1; Length 524;
Best Local Similarity 65.5%; Pred. No. 7e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSLSNAGHSDGPCNNNTSCLEFOPRGYECRDVNECDITEYCTGDSGCCPPLHK 55
Db 378 CULTHDMCSDGLCCRR--CKIEPRGVSCREAVNECDIAETCTGDSGCCPPLHK 430

RESULT 8
US-08-243-542-3
Sequence 3, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain CDNA library
US-08-243-542-3

Query Match 64.2%; Score 213; DB 1; Length 670;
Best Local Similarity 65.5%; Pred. No. 8.8e-14;
Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Oy 1 CSLNAGACSDGPCNNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
Db 378 CTLTHDAMCSDGLCCRR--CKYERGVSCRAVNECDIAETCTGDSGCCPPNLHK 430

RESULT 9

US-08-477-407-3
Sequence 3, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-477-407-3

Query Match 64.2%; Score 213; DB 1; Length 670;
Best Local Similarity 65.5%; Pred. No. 8.8e-14;

Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Oy 1 CSLNAGACSDGPCNNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
Db 378 CTLTHDAMCSDGLCCRR--CKYERGVSCRAVNECDIAETCTGDSGCCPPNLHK 430

RESULT 10

US-08-484-355-3
Sequence 3, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-484-355-3

Query Match 64.2%; Score 213; DB 1; Length 670;
Best Local Similarity 65.5%; Pred. No. 8.8e-14;

Matches 36; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

Oy 1 CSLNAGACSDGPCNNNTSCLFOPRGYECRDVAVNECDITEYCTGDSGCCPPNLHK 55
Db 378 CTLTHDAMCSDGLCCRR--CKYERGVSCRAVNECDIAETCTGDSGCCPPNLHK 430

Search completed: October 21, 2003, 10:12:26
Job time: 13.7987 secs

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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:06:05 ; Search time 24.2013 Seconds
(without alignments)
181.822 Million cell updates/sec

Title: US-09-634-252A-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTKLFEPTECGNGYVAGEE.....CPNLHKODGYACNONOGR 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 323717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*

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- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
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2	404.5	64.2	488	1 US-08-243-542-1	Sequence 1, Appli
3	404.5	64.2	488	1 US-08-477-407-1	Sequence 1, Appli
4	404.5	64.2	488	1 US-08-484-355-1	Sequence 1, Appli
5	404.5	64.2	524	1 US-08-243-542-2	Sequence 2, Appli
6	404.5	64.2	524	1 US-08-477-407-2	Sequence 2, Appli
7	404.5	64.2	524	1 US-08-484-355-2	Sequence 2, Appli
8	404.5	64.2	670	1 US-08-243-542-3	Sequence 3, Appli
9	404.5	64.2	670	1 US-08-477-407-3	Sequence 3, Appli
10	404.5	64.2	769	1 US-08-484-355-3	Sequence 3, Appli
11	404.5	64.2	769	1 US-08-243-542-4	Sequence 4, Appli
12	404.5	64.2	769	1 US-08-477-407-4	Sequence 4, Appli
13	404.5	64.2	769	1 US-08-484-355-4	Sequence 4, Appli
14	292	46.3	802	4 US-09-632-098-2	Sequence 2, Appli
15	292	46.3	812	4 US-09-632-098-4	Sequence 2, Appli
16	276.5	43.9	781	4 US-09-738-946-8	Sequence 8, Appli
17	274	43.5	814	3 US-09-813-819-4	Sequence 4, Appli
18	274	43.5	814	4 US-09-920-048-4	Sequence 4, Appli
19	274	43.5	855	3 US-09-813-819-2	Sequence 2, Appli
20	274	43.5	855	4 US-09-920-048-2	Sequence 2, Appli
21	263	41.7	621	4 US-09-026-001A-6	Sequence 6, Appli
22	259	41.1	613	4 US-09-026-001A-10	Sequence 10, Appli
23	259	41.1	621	4 US-09-026-001A-18	Sequence 18, Appli
24	257	40.8	751	2 US-08-836-443-3	Sequence 3, Appli
25	253.5	40.2	651	1 US-08-264-101-2	Sequence 2, Appli
26	253.5	40.2	651	1 US-08-765-243-2	Sequence 2, Appli
27	253.5	40.2	651	5 PCT-US95-07295-2	Sequence 2, Appli

28	253.5	40.2	734	2 US-08-765-243-8	Sequence 8, Appli
29	253.5	40.2	734	5 PCT-US95-07295-8	Sequence 8, Appli
30	252	40.0	616	4 US-09-608-790-1	Sequence 1, Appli
31	242	38.4	722	4 US-09-617-145-2	Sequence 2, Appli
32	215.5	34.2	462	4 US-09-026-001A-16	Sequence 16, Appli
33	209.5	33.3	457	1 US-08-264-101-4	Sequence 4, Appli
34	209.5	33.3	457	2 US-08-765-243-4	Sequence 4, Appli
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36	209.5	33.3	735	2 US-08-765-243-6	Sequence 6, Appli
37	209.5	33.3	735	5 PCT-US95-07295-6	Sequence 6, Appli
38	207.5	32.9	521	4 US-09-026-001A-12	Sequence 12, Appli
39	207.5	32.9	592	4 US-09-026-001A-14	Sequence 14, Appli
40	207	32.9	1239	2 US-08-937-931-2	Sequence 2, Appli
41	207	32.9	1239	3 US-08-937-931-2	Sequence 2, Appli
42	207	32.9	1239	4 US-09-285-502-2	Sequence 2, Appli
43	207	32.9	1239	4 US-09-709-126-2	Sequence 2, Appli
44	200.5	31.8	529	4 US-09-871-385A-2	Sequence 2, Appli
45	200.5	31.8	749	2 US-08-836-442-3	Sequence 3, Appli
				2 US-08-937-931-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-351-414-2
; Sequence 2, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Delisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISTINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-351-414-2

Query Match 100.0%; Score 630; DB 3; length 696;
Best local similarity 100.0%; Pred. No. 7.7e+45;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTKLFEPTECGNGYVAGEEBCDCGFHYECYGLCKCKSLSGAHCSDPCCNNTSCLP 60
Db 373 PTKLFEPTECGNGYVAGEEBCDCGFHYECYGLCKCKSLSGAHCSDPCCNNTSCLP 432

Qy 61 RGYCRDAVNECDITETCTGDSGCGCPNLHKODGYACNONOGR 104
Db 433 RGYCRDAVNECDITETCTGDSGCGCPNLHKODGYACNONOGR 476

RESULT 2
US-08-243-542-1
; Sequence 1, Application US/08243542
; Patent No. 5552526
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: EMI, MITSURU
; TITLE OF INVENTION: MDC PROTEINS AND DNAs
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA

```

1      ZIP: 49008-1699
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
4      COMPUTER: IBM PC/XT/AT Compatible
5      .OPERATING SYSTEM: MS-DOS 5.0
6      SOFTWARE: WordPerfect 5.0
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/08/243,542
9      FILING DATE:
10     CLASSIFICATION: 530
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: JP 5-136602
13     FILING DATE: 14 MAY 1993
14     APPLICATION NUMBER: JP 5-257455
15     FILING DATE: 22 SEPTEMBER 1993
16     APPLICATION NUMBER: JP 6-49904
17     FILING DATE: 23 FEBRUARY 1994
18     APPLICATION NUMBER: JP 6-73328
19     FILING DATE: 12 APRIL 1994
20     APPLICATION NUMBER: JP 6-84470
21     FILING DATE: 22 APRIL 1994
22     ATTORNEY/AGENT INFORMATION:
23     NAME: Terryence F. Chapman
24     REGISTRATION NUMBER: 32 549
25     REFERENCE/DOCKET NUMBER: Futuya Case 1313
26     TELECOMMUNICATION INFORMATION:
27     TELEPHONE: (616) 381-1156
28     TELEFAX: (616) 381-5465
29     INFORMATION FOR SEQ ID NO: 1:
30     SEQUENCE CHARACTERISTICS:
31     LENGTH: 488 amino acids
32     TYPE: amino acid
33     TOPOLOGY: linear
34     MOLECULE TYPE: protein
35     ORIGINAL SOURCE:
36     ORGANISM: Homo sapiens
37     IMMEDIATE SOURCE:
38     LIBRARY: human fecal brain cDNA library
39     US-08-243-542-1

```

	Query Match	Best Local Similarity	Matches	Score	DB 1	Length	488;
	64.2%	65.4%		404.5			
				Pred. No. 2.3e-26;			
			70; Conservative		9; Mismatches	23;	Indels 5; Gaps 2
Qy	1	PTKLEPPEPCNGGYVAGEECDCGFHVEY	---	GIQCKKCSISNMAHSGDSCGNNSTSL	57		
Db	332	PKLLDPPPCNGFVFAAGEECDCGSGVQEC	SRAGNCKKCKCITLTHDMGSDGLCCR	--CK	389		
Qy	58	FQPRRYECRDVAVNEDDITETCTGDSGQCP	PNLHKODGIA	CNONGRC	104		
Db	390	YEPKRVSCREAVNECDIAETCTGDSGQCP	PNLHKLDGYGCHDEGRNC		436		

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1  RESULT 3
2  US-08-477-407-1
3  : Sequence 1, Application US/08477407
4  : Patent No. 561351
5  : GENERAL INFORMATION:
6  : APPLICANT: NAKAMURA, YUSUKE
7  : APPLICANT: EMT, MITSURU
8  : TITLE OF INVENTION: MDC PROTEINS AND DNAS
9  : TITLE OF INVENTION: ENCODING THE SAME
10 : NUMBER OF SEQUENCES: 20
11 : CORRESPONDENCE ADDRESS:
12 : ADDRESSES: FLYNN, THIEL, BOUTELL & TANIS P.C.
13 : STREET: 2026 Rambling Road
14 : CITY: Kalamazoo
15 : STATE: Michigan
16 : COUNTRY: USA
17 : ZIP: 49008-1699
18 : COMPUTER READABLE FORM:
19 : MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
20 : COMPUTER: IBM PC/XT/AT Compatible

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? OPERATING SYSTEM: MS-DOS 5.0
? SOFTWARE: wordperfect 5.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/477,407
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 530
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: US 08/243,542
? FILING DATE: 13-MAY-1994
? APPLICATION NUMBER: JP 5-136602
? FILING DATE: 14 MAY 1993
? APPLICATION NUMBER: JP 5-257455
? FILING DATE: 22 SEPTEMBER 1993
? APPLICATION NUMBER: JP 6-49904
? FILING DATE: 23 FEBRUARY 1994
? APPLICATION NUMBER: JP 6-73328
? FILING DATE: 12 APRIL 1994
? APPLICATION NUMBER: JP 6-84470
? FILING DATE: 22 APRIL 1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Terryence F. Chapman
? REGISTRATION NUMBER: 32 549
? REFERENCE/DOCKET NUMBER: Furuwa Case 1313
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (616) 381-1156
? TELEFAX: (616) 381-5465
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 488 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? IMMEDIATE SOURCE:
? LIBRARY: human fetal brain cDNA library
US-08-477-407-1

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Query Match	64.2%	Score 404.5;	DB 1;	Length 488;
Best Local Similarity	65.4%;	Pred. No.2.3e-26;		
Matches	70;	Conservative 9;	Mismatches 23;	Indels 5; Gaps * 2.
QY	1	PTKLFEPBECNGVYEAGEECDGCFHVICY---GLCKCKCSLSNHAHSCDPECCNTSCL	57	
	:::::			
	:	:	:	:
Db	332	PLKLIDPECNGFVEAGEEBCDCDSVOECSPAGGCCCKCTLTTHAMCSDGLCCR--CK	389	
QY	58	FQPRGYECRDVAINECDITFEYCETGDSGOCPNLHKODGYACANONOGRC	104	
	:::::			
Db	390	YEPFGVSCREAVNECDIAETCTTGSSOCCPVLHKLDIYYCHDEGRC	436	

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1      RESULT 4
2      : Sequence 1, Application US/08484355
3      : Patent No. 5705341
4      :
5      : GENERAL INFORMATION:
6      : APPLICANT: NAKAMURA, YUSUKE
7      : APPLICANT: *EMI, MITSURU
8      : TITLE OF INVENTION: MDC PROTEINS AND DNAS
9      : TITLE OF INVENTION: ENCODING THE SAME
10     :
11     : NUMBER OF SEQUENCES: 20
12     :
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS P.C.
15     : STREET: 2026 Rambling Road
16     : CITY: Kalamazoo
17     : STATE: Michigan
18     :
19     : COUNTRY: USA
20     : ZIP: 49008-1699
21     :
22     : COMPUTER READABLE FORM:
23     : MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
24     : COMPUTER: IBM PC/XT/AT Compatible
25     : OPERATING SYSTEM: MS-DOS 5.0
26     : SOFTWARE: Wordperfect 5.0

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-484-355-1

Query Match      64.2%; Score 404.5; DB 1; Length 488;
Best Local Similarity 65.4%; Pred. No. 2.3e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy      1 PTKLFEPCNGNGVGECECDGCFHVECY--GLCKKCSLSKGAHCSGDPCCNNTSCL 57
Db      332 PLKLDPEPCNGNGVGECECDGSGVGECSRAGNCKKCTLTHTDAMCSDELCCRR--CK 389

Qy      58 FQPRGVECRDAVNECDITEYCTGDSGCCPPNLHKODGYACNQNGRC 104
Db      390 YEPRGVSCRAVNECDIAETCTGDSGCCPPNLHKLDGYCDHEQGR 436

RESULT 5
US-08-243-542-2
Sequence 2, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: MDC PROTEINS AND DNAs
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
```

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FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-243-542-2
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Query Match      64.2%; Score 404.5; DB 1; Length 524;
Best Local Similarity 65.4%; Pred. No. 2.3e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy      1 PTKLFEPCNGNGVGECECDGCFHVECY---GLCKKCSLSKGAHCSGDPCCNNTSCL 57
Db      339 PLKLDPEPCNGNGVGECECDGSGVGECSRAGNCKKCTLTHTDAMCSDELCCRR--CK 396

Qy      58 FQPRGVECRDAVNECDITEYCTGDSGCCPPNLHKODGYACNQNGRC 104
Db      397 YEPRGVSCRAVNECDIAETCTGDSGCCPPNLHKLDGYCDHEQGR 443

RESULT 6
US-08-477-407-2
Sequence 2, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: MDC PROTEINS AND DNAs
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
```

FILED DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILED DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILED DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILED DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILED DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILED DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-477-407-2

Query Match 64.2%; Score 404.5; DB 1; Length 524;
Best Local Similarity 65.4%; Pred. No. 2.5e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLEPPEPCNGGYEAGEECDCGFHVECY---GLCKKCSLSNGAHGSDGPCNNNTSCL 57
Db 339 PTKLEPPEPCNGGYEAGEECDCGVSQVBCSRAGNCKCKCTLTHDMCSDGLCCRR--CK 396
Qy 58 FQPRGECRDVAVNECDITEYCTGDSGQCPNHLHKODGYACNONGRC 104
Db 397 YEPRGVSCRAVNECDIAETCTGDSGQCPNHLHKLDGYCHDHEGRC 443

RESULT 7
US-08-484-355-2
Sequence 2, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILED DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILED DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602

FILED DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILED DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILED DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILED DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILED DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-484-355-2

Query Match 64.2%; Score 404.5; DB 1; Length 524;
Best Local Similarity 65.4%; Pred. No. 2.5e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLEPPEPCNGGYEAGEECDCGFHVECY---GLCKKCSLSNGAHGSDGPCNNNTSCL 57
Db 339 PTKLEPPEPCNGGYEAGEECDCGVSQVBCSRAGNCKCKCTLTHDMCSDGLCCRR--CK 396
Qy 58 FQPRGECRDVAVNECDITEYCTGDSGQCPNHLHKODGYACNONGRC 104
Db 397 YEPRGVSCRAVNECDIAETCTGDSGQCPNHLHKLDGYCHDHEGRC 443

RESULT 8
US-08-243-542-3
Sequence 3, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILED DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILED DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILED DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904

FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-243-542-3

Query Match 64.2%; Score 404.5; DB 1; Length 670;
Best Local Similarity 65.4%; Pred. No. 3.1e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;
QY 1 PRTLFPTECGNGYVAGEECDCGPFHYECY---GLCKKCSLSNGAHGSDGPCNNNTSCL 57
DB 339 PLKLDLPPECGNGFVAGEECDCGSGVQECBRAGNCCCKCTLTHDMCSDGLCCRR--CK 396
QY 58 FQPRGYECRDVAVNECDITEYCTGDSGQCPNHLKHODGYACNONGRC 104
DB 397 YEPRGVSCRAVAVNECDIAETCTGDSQCPNHLKLDGYCDHOGRC 443

RESULT 9
US-08-477-407-3
Sequence 3, Application US/08477407
Patent No. 563351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328

FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 670 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
US-08-477-407-3

Query Match 64.2%; Score 404.5; DB 1; Length 670;
Best Local Similarity 65.4%; Pred. No. 3.1e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;
QY 1 PRTLFPTECGNGYVAGEECDCGPFHYECY---GLCKKCSLSNGAHGSDGPCNNNTSCL 57
DB 339 PLKLDLPPECGNGFVAGEECDCGSGVQECBRAGNCCCKCTLTHDMCSDGLCCRR--CK 396
QY 58 FQPRGYECRDVAVNECDITEYCTGDSGQCPNHLKHODGYACNONGRC 104
DB 397 YEPRGVSCRAVAVNECDIAETCTGDSQCPNHLKLDGYCDHOGRC 443

RESULT 10
US-08-484-355-3
Sequence 3, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
APPLICATION NUMBER: JP 6-84470

```

; FILING DATE: 22 APRIL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Terryence F. Chapman
; REGISTRATION NUMBER: 32 549
; REFERENCE/DOCKET NUMBER: Furuya Case 1313
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 381-1156
; TELEFAX: (616) 381-5465
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 670 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: human fetal brain cDNA library
; US-08-484-355-3

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Query Match 64.2%; Score 404.5; DB 1; Length 670;
Best Local Similarity 65.4%; Pred. No. 3.1e-26;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

OY 1 PTKLPEPTGCGNGYEAGEECDCGFHVECY--GLCKKCSLSNGAHGSDGPPCCNNTSCL 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 339 PLKLDPEPCGNGFVEAGEECDCGSGVQECSPRAGNCKCKKTLTHDAMCSDGLCCRR--CK 396
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 58 FQPRGYEGRDAVNECDITEYCTGDSGCGCPNLHKODGYACNONGRC 104
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 397 YEPNGVSCREAVNECDIAETCTGDSGCGCPNLHKLDGYCDHEGRC 443
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Search completed: October 21, 2003, 10:12:25
 Job time : 25.2013 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 21, 2003, 10:20:51 ; Search time 62.1384 Seconds
(without alignments)
738.736 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599

Sequence: 1 PRTLPFPTCEGNGYVEAGE.....CPNHLKHQDQVACNQNGRC 104

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xjh
-Q=/cgn2_1/USFTO.spool/US09634252/rnat_21102003_090325_34C1/app_query.fasta_1.462
-DB=Issued_Patents_NA -OPMT=faflatp -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=10
-MODE=LOCAL -OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09634252.CCN 1.1 76 @rnat_21102003_090325_3401 -NCPU=6 -ICPU=3
-NO_MAP -JARSBQTRY -NEG_SCORES=0 -WAIT -DSFBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

- Issued Patents NA.*
1: /cgn2_6/pctdata/2/ina/5A.COMB.seq.*
2: /cgn2_6/pctdata/2/ina/5B.COMB.seq.*
3: /cgn2_6/pctdata/2/ina/6A.COMB.seq.*
4: /cgn2_6/pctdata/2/ina/6B.COMB.seq.*
5: /cgn2_6/pctdata/2/ina/6C.COMB.seq.*
6: /cgn2_6/pctdata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	630	100.0	2268	3	US-09-351-414-1 Sequence 1, Appli
2	567	90.0	2088	3	US-09-351-414-3 Sequence 3, Appli
3	404.5	64.2	1464	1	US-08-243-542-5 Sequence 5, Appli
4	404.5	64.2	1464	1	US-08-477-407-5 Sequence 5, Appli
5	404.5	64.2	1464	1	US-08-484-355-5 Sequence 5, Appli
6	404.5	64.2	2913	1	US-08-243-542-7 Sequence 7, Appli
7	404.5	64.2	2913	1	US-08-477-407-7 Sequence 7, Appli
8	404.5	64.2	2913	1	US-08-484-355-7 Sequence 7, Appli
9	404.5	64.2	2923	1	US-08-243-542-6 Sequence 6, Appli
10	404.5	64.2	2923	1	US-08-477-407-6 Sequence 6, Appli
11	404.5	64.2	2923	1	US-08-484-355-6 Sequence 6, Appli
12	404.5	64.2	3183	1	US-08-243-542-8 Sequence 8, Appli

13	404.5	64.2	3183	1	US-08-477-407-8 Sequence 8, Appli
14	404.5	64.2	3183	1	US-08-484-355-8 Sequence 8, Appli
15	292	46.3	3431	1	US-09-632-098-1 Sequence 1, Appli
16	292	46.3	3468	4	US-09-632-098-3 Sequence 3, Appli
17	276.5	43.9	3984	4	US-09-738-946-7 Sequence 7, Appli
18	274	43.5	2968	3	US-09-813-819-1 Sequence 1, Appli
19	274	43.5	2968	4	US-09-920-048-1 Sequence 1, Appli
20	265	42.1	2406	4	US-09-632-098-5 Sequence 5, Appli
21	265	42.1	2439	4	US-09-632-098-6 Sequence 6, Appli
22	263	41.7	2050	4	US-09-026-001A-5 Sequence 5, Appli
23	259	41.1	2335	4	US-09-026-001A-9 Sequence 9, Appli
24	259	41.1	2339	4	US-09-026-001A-17 Sequence 17, Appli
25	257	40.8	2251	2	US-08-836-443-2 Sequence 2, Appli
26	257	40.8	2648	2	US-08-836-443-7 Sequence 7, Appli
27	255	40.5	1463	5	PCT-US93-05640-10 Sequence 10, Appli
28	253.5	40.2	2373	1	US-08-765-243-1 Sequence 1, Appli
29	253.5	40.2	2373	2	US-08-765-243-1 Sequence 1, Appli
30	253.5	40.2	2373	5	PCT-US95-07295-1 Sequence 1, Appli
31	253.5	40.2	2650	2	US-08-765-243-7 Sequence 7, Appli
32	253.5	40.2	2650	5	PCT-US95-07295-7 Sequence 7, Appli
33	252	40.0	1851	4	US-09-608-790-2 Sequence 2, Appli
34	242	38.4	2169	4	US-09-617-145-1 Sequence 1, Appli
35	215.5	34.2	1820	4	US-09-026-001A-15 Sequence 15, Appli
36	211	33.5	1550	2	US-08-836-442-2 Sequence 2, Appli
37	211	33.5	2056	2	US-08-836-442-1 Sequence 1, Appli
38	209.5	33.3	1768	1	US-08-264-101-3 Sequence 3, Appli
39	209.5	33.3	1768	2	US-08-765-243-3 Sequence 3, Appli
40	209.5	33.3	1768	5	PCT-US95-07295-3 Sequence 3, Appli
41	209.5	33.3	2553	2	US-08-765-243-5 Sequence 5, Appli
42	209.5	33.3	2553	5	PCT-US95-07295-5 Sequence 5, Appli
43	207.5	32.9	2288	4	US-09-026-001A-11 Sequence 11, Appli
44	207.5	32.9	2309	4	US-09-026-001A-13 Sequence 13, Appli
45	207	32.9	5630	2	US-08-937-931-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-351-414-1
Sequence 1, Application US/09351414
Patent No. 6265199
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Beinbur, Nand
APPLICANT: Deisher, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351.414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ. ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(2090)
NAME/KEY: misc_feature
LOCATION: (1)...(2268)
OTHER INFORMATION: n = A,T,C or G
US-09-351-414-1

Alignment Scores:

Pred. No.: 2.17e-63 Length: 2268
Score: 630.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-634-252a-4_COPY_496_599 (1-104) x US-09-351-414-1 (1-2268)

QY 1 ProThrIlyLeuPheGluProThrGluCysGlyAsnGlyTYrValGluAlaGlyGluGlu 20
DB 1119 CCAACAAAGCTATTGAGCCCAACGGAATGTGAATGATAGCTGGAAGCTGGGAGAG 1178
QY 21 CysAspCysGlyPheHisValGluCysTYrGlyLeuCysValGlySerSerLeuSer 40
DB 1179 TGTGATTTGTGTTTTCATGCTGGAATGCTATGATATTGCTGTAAGAAATGTTCCCTCTCC 1238
QY 41 AenGlyAlaHisCysSerAspGlyProCysCysAsnAenThrSerCysLeuPheGlnPro 60
DB 1229 AACGGGCTCACTGACGACGACGCGCCCTGCTGTAACATACCTCATGCTTTTTCAGCCA 1298
QY 61 ArgGlyTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTYrCysThrGly 80
DB 1299 CGAGGATATGAATGCCGGGATGCTGTGAACGAGTGTGATATTACTGAATATTGTACTGGA 1358
QY 81 AspSerGlyGlnCysProProAsnLeuHisIlyGlnAspGlyTYrAlaCysAsnGlnAsn 100
DB 1359 GACTGTGTCAGTGCACCAAAATCTTCTAAGCAAGCGATATGCAATGCAATCAAAAT 1418
QY 101 GlnGlyArgCys 104
DB 1419 CAGGCGCTGCTC 1430
QY 1419 CAGGCGCTGCTC 1430
DB 1419 CAGGCGCTGCTC 1430
RESULT 2
US-09-351-414-3
; Sequence 3, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Baldwin, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2088
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zdn1 amino acid degenerate sequence
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(2088)
; OTHER INFORMATION: n is any nucleotide
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)_(2088)
; OTHER INFORMATION: n = A,T,C or G
US-09-351-414-3
Alignment Scores:
Pred. No.: 3,77e-56 Length: 2088
Score: 567.00 Matches: 91
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 13
Query Match: 90.00% Indels: 0
DB: 3 Gaps: 0
US-09-634-252A-4_COPY_496_599 (1-104) x US-09-351-414-3 (1-2088)
QY 1 ProThrIlyLeuPheGluProThrGluCysGlyAsnGlyTYrValGluAlaGlyGluGlu 20
DB 1117 CCNACNAARYTNTTTCAGRCNACNGARCTGCGNAAYGCGTATGTCGARGCNGCNGARGAR 1176
QY 21 CysAspCysGlyPheHisValGluCysTYrGlyLeuCysValGlySerSerLeuSer 40
DB 1177 TGTGATTTGTGTTTTCATGCTGGAATGCTATGATATTGCTGTAAGAAATGTTCCCTCTCC 1236

QY 41 AenGlyAlaHisCysSerAspGlyProCysCysAsnAenThrSerCysLeuPheGlnPro 60
DB 1227 AATGNGCNCATGTGWSGALGNCNCNTGTYGTAAYAAACMSNTGTYTTTTCARCCN 1296
QY 61 ArgGlyTYrGluCysArgAspAlaValAsnGluCysAspIleThrGluTYrCysThrGly 80
DB 1297 MNGGNTAYGARTGWMGAGVGCNGTNAAYGARTGYGAYATGACGARTATGVAACNGCN 1356
QY 81 AspSerGlyGlnCysProProAsnLeuHisIlyGlnAspGlyTYrAlaCysAsnGlnAsn 100
DB 1357 GAYWSNGNCARTGTCNCNCAAYTNCAYARCARGAYGNTAYGCVNTGYAAACARAA 1416
QY 101 GlnGlyArgCys 104
DB 1417 CARGGNGMTGT 1428
RESULT 3
US-08-243-542-5
; Sequence 5, Application US/08243542
; Patent No. 5552526
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: : EMI, MITSURU
; TITLE OF INVENTION: MDC PROTEINS AND DNAs
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLYNN, THEL, BOUTELL & TANIS P.C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,542
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-136602
; FILING DATE: 14 MAY 1993
; APPLICATION NUMBER: JP 5-257455
; FILING DATE: 22 SEPTEMBER 1993
; APPLICATION NUMBER: JP 6-49904
; FILING DATE: 23 FEBRUARY 1994
; APPLICATION NUMBER: JP 6-73328
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: JP 6-84470
; FILING DATE: 22 APRIL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Terryence F. Chapman
; REGISTRATION NUMBER: 32 549
; REFERENCE/DOCKET NUMBER: Puruya Case 1313
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 381-1156
; TELEFAX: (616) 381-5465
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: human fetal brain cDNA library
; FEATURE:

NAME/KEY: CDS
LOCATION: 1..1464
US-08-243-542-5

Alignment Scores:
Pred. No.: 1,47e-37 Length: 1464
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-08-243-542-5 (1-1464)

Qy 1 ProthrllysluPheglupProthrgluCyasglYasnlglyTyra1glua1aglglu1u 20
Db 994 CCCCTCAAGCTCTCTGAGACCCCGAGAGTGGGAAACGGCTTCGTGAGAGCGGGAGAG 1053

Qy 21 CysAspCysglYphen1svalgluCystrY-----glyLeuCyCylyslYsCys 37
Db 1054 TGGCAGTGGCGGCTGGGTCAGAGAGTGGCAGCGCGCAGGTGGCAATGCTGCAAGAAATGC 1113

Qy 38 SerleuSerasnlgly1ah1sCysSerAspglYProCyCySasnlnrThrSerCysleu 57
Db 1114 ACCCTGACTCAGACGCGCATGTGCAGCGACGCGGCTCTGCTGCG:CGC-----TGCAG 1167

Qy 58 PheglNProArgrglYTyrgluCyArgrAspAlavalasnlglyCyAspIleThrgluTyx 77
Db 1168 TACCAACACCGGGGTGTCTCTCTGCGAGAGCGCGGAAACGAGTGCACATGCGGAGACC 1227

Qy 78 CysThrglyAspserglYglncYsPProAsnleuh1slysglnaefglYTyra1aCys 97
Db 1228 TGCACCGGGGACTTACGCAAGTGGCCGCTTAACCTGCACAGCTGCAGGTTACTACTGT 1287

Qy 98 AsnclnAsnlglnlglyArgrCys 104
Db 1288 GACCATGAGCAGGCGCGCTGC 1308

RESULT 4
US-08-477-407-5
Sequence 5, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994

APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Teriyence F. Chapman
REGISTRATION/DOCKET NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1464
US-08-477-407-5

Alignment Scores:
Pred. No.: 1,47e-37 Length: 1464
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-08-477-407-5 (1-1464)

Qy 1 ProthrllysluPheglupProthrgluCyasglYasnlglyTyra1glua1aglglu1u 20
Db 994 CCCCTCAAGCTCTCTGAGACCCCGAGAGTGGGAAACGGCTTCGTGAGAGCGGGAGAG 1053

Qy 21 CysAspCysglYphen1svalgluCystrY-----glyLeuCyCylyslYsCys 37
Db 1054 TGGCAGTGGCGGCTGGGTCAGAGAGTGGCAGCGCGCAGGTGGCAATGCTGCAAGAAATGC 1113

Qy 38 SerleuSerasnlgly1ah1sCysSerAspglYProCyCySasnlnrThrSerCysleu 57
Db 1114 ACCCTGACTCAGACGCGCATGTGCAGCGACGCGGCTCTGCTGCGCGC-----TGCAG 1167

Qy 58 PheglNProArgrglYTyrgluCyArgrAspAlavalasnlglyCyAspIleThrgluTyx 77
Db 1168 TACCAACACCGGGGTGTCTCTCTGCGAGAGCGCGGAAACGAGTGCACATGCGGAGACC 1227

Qy 78 CysThrglyAspserglYglncYsPProAsnleuh1slysglnaefglYTyra1aCys 97
Db 1228 TGCACCGGGGACTTACGCAAGTGGCCGCTTAACCTGCACAGCTGCAGGTTACTACTGT 1287

Qy 98 AsnclnAsnlglnlglyArgrCys 104
Db 1288 GACCATGAGCAGGCGCGCTGC 1308

RESULT 5
US-08-484-355-5
Sequence 5, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.

NAME/KEY: CDS
LOCATION: 28..2037
US-08-243-542-7

Alignment Scores:
Pred. No.: 3,74e-37 Length: 2913
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-08-243-542-7 (1-2913)

QY 1 ProThrlYsleuPhheGluProThrgluCyGlyAsnGlyTyrValGluAlaGluGlu 20
Db 1042 CCCCTCAAGCTCTTGAGACCCCGAGAGTGGGGAACGGCTTCTGAGAGGAGGAGAG 1101

QY 21 CysAspCysGlyPheHisValGluCysTyr-----GlyLeuCysCysLysLysCys 37
Db 1102 TGGGACTGGCGGCTCGGTGACAGAGTGACGCCGACAGTGCAACTGCTCCAGAAATGC 1161

QY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnThrSerCysLeu 57
Db 1162 ACCCTGACTCAGCAGCCGATGTGACGAGCGGCTGTGTCGCC-----TGCAG 1215

QY 58 PheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyr 77
Db 1216 TACGAACACGAGGAGGTGTCTCTCCGAGAGCGCTGACACAGTGCACATCGCGAGACC 1275

QY 78 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCys 97
Db 1276 TGCACCGGGGACTCTAGCCAGTGCAGCGCCCTAACCTGCAAGCTGCAGCGTTACTACTGT 1335

QY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1336 GACCATGAGCAGGCGCGCTGC 1356

RESULT 7
US-08-477-407-7
Sequence 7, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
City: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994

APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2913 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library

FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..27
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 2038..2913
FEATURE:
NAME/KEY: CDS
LOCATION: 28..2037
US-08-477-407-7

Alignment Scores:
Pred. No.: 3,74e-37 Length: 2913
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-08-477-407-7 (1-2913)

QY 1 ProThrlYsleuPhheGluProThrgluCyGlyAsnGlyTyrValGluAlaGluGlu 20
Db 1042 CCCCTCAAGCTCTTGAGACCCCGAGAGTGGGGAACGGCTTCTGAGAGGAGGAGAG 1101

QY 21 CysAspCysGlyPheHisValGluCysTyr-----GlyLeuCysCysLysLysCys 37
Db 1102 TGGGACTGGCGGCTCGGTGACAGAGTGACGCCGACAGTGCAACTGCTCCAGAAATGC 1161

QY 38 SerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnThrSerCysLeu 57
Db 1162 ACCCTGACTCAGCAGCCGATGTGACGAGCGGCTGTGTCGCC-----TGCAG 1215

QY 58 PheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGluTyr 77
Db 1216 TACGAACACGAGGAGGTGTCTCTCCGAGAGCGCTGACACAGTGCACATCGCGAGACC 1275

QY 78 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAlaCys 97
Db 1276 TGCACCGGGGACTCTAGCCAGTGCAGCGCCCTAACCTGCAAGCTGCAGCGTTACTACTGT 1335

QY 98 AsnGlnAsnGlnGlyArgCys 104
Db 1336 GACCATGAGCAGGCGCGCTGC 1356

RESULT 8
US-08-484-355-7
Sequence 7, Application US/08484355
Patent No. 570341
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE

APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THEIL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2913 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..27
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 2038..2913
FEATURE:
NAME/KEY: CDS
LOCATION: 28..2037
US-08-484-355-7
Alignment Scores:
Pred. No.: 3.74e-37 Length: 2913
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2
US-09-634-252a-4_COPY_496_599 (1-104) x US-08-484-355-7 (1-2913)
QY 1 ProthrllysLeupheglupProthrglucysgluysnglyTyrrvalglualglgylnglu 20

Db 1042 CCCCTCAAGCTCTCGAGACCCCGGAGAGTGGCGAAGCGCTTCGTGAGGCGAGGAGAG 1101
QY 21 CysAspCysGlyPheHisValGluCysTyr-----GlyLeuCysCysValCysCys 37
Db 1102 TGCAGCTGGGCTGGGTGGAGAGTGAAGCGCCGAGGTGCACACTGCTGCAAGAAATGC 1161
QY 38 SerLeuSerAenGlyAlaHisCysSerAspGlyProCysCysAsnAsnThSerCysLeu 57
Db 1162 ACCCTGACTCAGACGCGCATGTGACGAGCGCGGCTGCTGTCCCGC-----TGCAG 1215
QY 58 PheGlnProAlaGlyTyrrGluCysArgAspAlaValAsnGluCysAspIleThGluTyr 77
Db 1216 TACGAGACCGGGGTGTCTCTCGCCGAGAGCGCGTGAACGAGTGCACATCGCGAGACC 1275
QY 78 CysThrGlyAspSerGlyGlnCysProProAsnLeuHisValAsnGluCysAspIleThGluTyr 97
Db 1276 TGCACCGGGGACTCTAGCCAGTGGCCGCTTAACCTGCACAGCTGAGCGTTACTACTGT 1335
QY 98 AsnGlnAenGlnGlyArgCys 104
Db 1336 GACCATGACGAGGCGCGCTGC 1356
RESULT 9
US-08-243-542-6
Sequence 6, Application US/08243542
Patent No. 5552526
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THEIL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Futuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..27
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 1600..2923
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1599
US-08-243-542-6

Alignment Scores:
Pred. No.: 3,75e-37 Length: 2923
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-08-243-542-6 (1..2923)

Qy 1 ProthrylsleuphegipProthrgluCyseglYasnglyTYrValgluAlaGlygluGlu 20
Db 1042 CCCCTCAAGCTCTCGGACCCCCCAGAGTGCAGGAAACGGCTTCGKAGCGCGAGGAGAG 1101

Qy 21 CysAapCyseglYphenisValgluCyseTYr-----GlyLeuCyseYsLysCyse 37
Db 1102 TGGACACTGCGGCTCGTGAGAGAGTGCAGCGCCGAGGTGGCAKTCGTGCAGAAATGC 1161

Qy 38 SerleuseraenglyAlaHisCyseSerAapglyProCyseYsaAnaentTherCyseleu 57
Db 1162 ACCCTGACTCAGCAGCGCATGTGCAGCGACGGCTCTGCTCCGCC-----TGCAG 1215

Qy 58 PheglProaraglyTYrGluCyseArgAspAlaValaengluCyseAapIleThrGluTYr 77
Db 1216 TACCAACACAGGGGTGTCTCTCGGAGAGGCCCTGAACGAGTGCACATCGCGAGACC 1275

Qy 78 CysThrglyAapSerGlyInCyseProProAanleuHisLysgluAapglyTYrAlaCyse 97
Db 1276 TGCACCGGGGACTCTAGCAGAGTGCAGCGCTACCTGCAACAGCTKAGCGTTACTACTGT 1335

Qy 98 AenglnAenglnglyAArgCyse 104
Db 1336 GACCATGAGCAGGCGCGCTGC 1356

RESULT 10
US-08-477-407-6
Sequence 6, Application US/08477407
Patent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAs
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PLYNN, THIEL, BOUTELL & TANIS P. C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Furuya Case 1313
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..27
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 1600..2923
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1599
US-08-477-407-6

Alignment Scores:
Pred. No.: 3,75e-37 Length: 2923
Score: 404.50 Matches: 70
Percent Similarity: 73.83% Conservative: 9
Best Local Similarity: 65.42% Mismatches: 23
Query Match: 64.21% Indels: 5
DB: 1 Gaps: 2

US-09-634-252a-4_COPY_496_599 (1-104) x US-08-477-407-6 (1..2923)

Qy 1 ProthrylsleuphegipProthrgluCyseglYasnglyTYrValgluAlaGlyglu 20
Db 1042 CCCCTCAAGCTCTCGGACCCCCCAGAGTGCAGGAAACGGCTTCGKAGCGCGAGGAGAG 1101

Qy 21 CysAapCyseglYphenisValgluCyseTYr-----GlyLeuCyseYsLysCyse 37
Db 1102 TGGACACTGCGGCTCGTGAGAGAGTGCAGCGCCGAGGTGGCAKTCGTGCAGAAATGC 1161

Qy 38 SerleuseraenglyAlaHisCyseSerAapglyProCyseYsaAnaentTherCyseleu 57
Db 1162 ACCCTGACTCAGCAGCGCATGTGCAGCGACGGCTCTGCTCCGCC-----TGCAG 1215

Qy 58 PheglProaraglyTYrGluCyseArgAspAlaValaengluCyseAapIleThrGluTYr 77
Db 1216 TACCAACACAGGGGTGTCTCTCGGAGAGGCCCTGAACGAGTGCACATCGCGAGACC 1275

Qy 78 CysThrglyAapSerGlyInCyseProProAanleuHisLysgluAapglyTYrAlaCyse 97
Db 1336 GACCATGAGCAGGCGCGCTGC 1356

Db 1276 TGCACCGGGGACTTAGCCAGTGCCCCGCTTAAGTGCACAGAGCTGACGGTTACTACTGT 1335
Qy 98 AsnglnAsnglnGlyArgCys 104
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Db 1336 GACCATGAGCAGCGCGCTGC 1356

Search completed: October 21, 2003, 12:03:42
Job time : 68.1384 secs